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Figure 1: 158P1D7 SSH sequence (SEQ ID NO: 1).

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1  GATCTGATAA GCTTTCAATG TTGCGCTCCT GACAATGTAT TAGAAGTCCT GATGGGGATA
61 GGACTTTGCA GTTACAAGGA ATAGGGCAGA AAGGTCCTGG AAGTTGAGTG GATGGCTTTG
121 TAATATAAGG TATCAAACCT GGTGCTTTGG TGGGTAGTTT TAGAATGGAC GTGGTCTTAG
181 TTGACATGCG ACTATCATTT ATTGAAGATG TTGCTGCCAG ATGTAATGAT C
```

Figure 2:

Figure 2A. The cDNA (SEQ ID NO: 2) and amino acid sequence (SEQ ID NO: 3) of 158P1D7 v.1.

The start methionine is underlined. The open reading frame extends from nucleic acid 23-2548 including the stop codon.

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1           M K L W I H L F Y S S L L
1 tcggatttcatcacatgacaacATGAAGCTGTGGATTCATCTCTTTTATTCATCTCTCCT
14  A C I S L H S Q T P V L S S R G S C D S
61 TGCCTGTATATCTTTACTCTCCAACTCCAGTGCTCTCATCCAGAGGCTCTTGTGATTC
34  L C N C E E K D G T M L I N C E A K G I
121 TCTTTGCAATTGTGAGGAAAAAGATGGCACAATGCTAATAAATTGTGAAGCAAAGGTAT
54  K M V S E I S V P P S R P F Q L S L L N
181 CAAGATGGTATCTGAAATAAGTGTGCCACCATCACGACCTTCCAACTAAGCTTATTAAA
74  N G L T M L H T N D F S G L T N A I S I
241 TAACGGCTTGACGATGCTTCACACAAATGACTTTTCTGGGCTTACCAATGCTATTTCAAT
94  H L G F N N I A D I E I G A F N G L G L
301 ACACCTTGGATTTAACAATATTGCAGATATTGAGATAGGTGCATTTAATGGCCTTGGCCT
114 L K Q L H I N H N S L E I L K E D T F H
361 CCTGAAACAACTTCATATCAATCACAATTCTTTAGAAATTCTTAAAGAGGATACTTTCCA
134 G L E N L E F L Q A D N N F I T V I E P
421 TGGACTTGAAAACCTGGAATTCCTGCAAGCAGATAACAATTTTATCACAGTGATTGAACC
154 S A F S K L N R L K V L I L N D N A I E
481 AAGTGCCTTTAGCAAGCTCAACAGACTCAAAGTGTTAATTTTAAATGACAATGCTATTGA
174 S L P P N I F R F V P L T H L D L R G N
541 GAGTCTTCCTCCAAACATCTTCCGATTGTTCCTTTAACCCATCTAGATCTTCGTGGAAA
194 Q L Q T L P Y V G F L E H I G R I L D L
601 TCAATTACAAACATTGCCTTATGTTGGTTTCTCGAACACATTGGCCGAATATTGGATCT
214 Q L E D N K W A C N C D L L Q L K T W L
661 TCAGTTGGAGGACAACAAATGGGCCTGCAATTGTGACTTATTGCAGTTAAAACTTGGTT
234 E N M P P Q S I I G D V V C N S P P F F
721 GGAGAACATGCCTCCACAGTCTATAATTGGTGATGTTGTCTGCAACAGCCCTCCATTTTT
254 K G S I L S R L K K E S I C P T P P V Y
781 TAAAGGAAGTATACTCAGTAGACTAAAGAAGGAATCTATTTGCCCTACTCCACCAGTGTA
274 E E H E D P S G S L H L A A T S S I N D
841 TGAAGAACATGAGGATCCTTCAGGATCATTACATCTGGCAGCAACATCTTCAATAAATGA
294 S R M S T K T T S I L K L P T K A P G L
901 TAGTCGCATGTCAACTAAGACCAGTCCATTCTAAACTACCCACCAAAGCACCAGGTTT
314 I P Y I T K P S T Q L P G P Y C P I P C
961 GATACCTTATATTACAAAGCCATCCACTCAACTTCCAGGACCTTACTGCCCTATTCTTG
334 N C K V L S P S G L L I H C Q E R N I E
1021 TAACTGCAAAGTCCTATCCCCATCAGGACTTCTAATACATTGTCAGGAGCGCAACATTGA
354 S L S D L R P P P Q N P R K L I L A G N

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1081 AAGCTTATCAGATCTGAGACCTCCTCCGCAAAATCCTAGAAAGCTCATTCTAGCGGGAAA
374 I I H S L M K S D L V E Y F T L E M L H
1141 TATTATTCACAGTTTAATGAAGTCTGATCTAGTGAATATTTCACTTTGGAAATGCTTCA
394 L G N N R I E V L E E G S F M N L T R L
1201 CTTGGGAAACAATCGTATTGAAGTTCTTGAAGAAGGATCGTTTATGAACCTAACGAGATT
414 Q K L Y L N G N H L T K L S K G M F L G
1261 ACAAAAACCTCTATCTAAATGGTAACCACTGACCAAATTAAGTAAAGGCATGTTCTTGG
434 L H N L E Y L Y L E Y N A I K E I L P G
1321 TCTCCATAATCTTGAATACTTATATCTTGAATACAATGCCATTAAGGAAATACTGCCAGG
454 T F N P M P K L K V L Y L N N N L L Q V
1381 AACCTTTAATCCAATGCCTAACTTAAAGTCCTGTATTTAAATAACAACCTCCTCCAAGT
474 L P P H I F S G V P L T K V N L K T N Q
1441 TTTACCACCACATATTTTTTCAGGGGTTCTCTAACTAAGGTAAATCTTAAAACAAACCA
494 F T H L P V S N I L D D L D L L T Q I D
1501 GTTTACCCATCTACCTGTAAGTAATATTTTGATGATCTTGATTACTAATCCAGATTGA
514 L E D N P W D C S C D L V G L Q Q W I Q
1561 CCTTGAGGATAACCCCTGGGACTGCTCCTGTGACCTGGTTGGACTGCAGCAATGGATACA
534 K L S K N T V T D D I L C T S P G H L D
1621 AAAGTTAAGCAAGAACACAGTGACAGATGACATCCTCTGCACTTCCCCCGGCATCTCGA
554 K K E L K A L N S E I L C P G L V N N P
1681 CAAAAAGGAATTGAAAGCCCTAAATAGTGAAATTCTCTGTCCAGGTTTAGTAAATAACCC
574 S M P T Q T S Y L M V T T P A T T T N T
1741 ATCCATGCCAACACAGACTAGTTACCTTATGGTCACCACTCCTGCAACAACAACAATAC
594 A D T I L R S L T D A V P L S V L I L G
1801 GGCTGATACTATTTTACGATCTCTTACGGACGCTGTGCCACTGTCTGTTCTAATATTGGG
614 L L I M F I T I V F C A A G I V V L V L
1861 ACTTCTGATTATGTTTCATCACTATTGTTTCTGTGCTGCAGGGATAGTGGTTCTTGTCT
634 H R R R R Y K K K Q V D E Q M R D N S P
1921 TCACCGCAGGAGAAGATACAAAAAGAAACAAGTAGATGAGCAAATGAGAGACAACAGTCC
654 V H L Q Y S M Y G H K T T H H T T E R P
1981 TGTGCATCTTCAGTACAGCATGTATGGCCATAAAACCACTCATCACTACTGAAAGACC
674 S A S L Y E Q H M V S P M V H V Y R S P
2041 CTCTGCCTCACTCTATGAACAGCACATGGTGAGCCCCATGGTTCATGTCTATAGAAGTCC
694 S F G P K H L E E E E E R N E K E G S D
2101 ATCCTTTGGTCCAAAGCATCTGGAAGAGGAAGAAGAGAGGAATGAGAAAGAAGGAAGTGA
714 A K H L Q R S L L E Q E N H S P L T G S
2161 TGCAAAACATCTCCAAAGAAGTCTTTTGGAAACAGGAAAATCATTCACTACTACAGGGTC
734 N M K Y K T T N Q S T E F L S F Q D A S
2221 AAATATGAAATACAAAACCACGAACCAATCAACAGAATTTTTATCCTTCCAAGATGCCAG
754 S L Y R N I L E K E R E L Q Q L G I T E
2281 CTCATTGTACAGAAACATTTTAGAAAAAGAAAGGGAACCTCAGCAACTGGGAATCACAGA
774 Y L R K N I A Q L Q P D M E A H Y P G A

2341 ATACCTAAGGAAAAACATTGCTCAGCTCCAGCCTGATATGGAGGCACATTATCCTGGAGC
794 H E E L K L M E T L M Y S R P R K V L V
2401 CCACGAAGAGCTGAAGTTAATGGAAACATTAATGTACTCACGTCCAAGGAAGGTATTAGT
814 E Q T K N E Y F E L K A N L H A E P D Y
2461 GGAACAGACAAAAAATGAGTATTTTGAAGCTTAAAGCTAATTTACATGCTGAACCTGACTA
834 L E V L E Q Q T *
2521 TTTAGAAGTCCTGGAGCAGCAAACATAGatggaga

Figure 2B. The cDNA (SEQ ID NO: 4) and amino acid sequence (SEQ ID NO: 5) of 158P1D7 v.2.
The start methionine is underlined. The open reading frame extends from nucleic acid 23-2548 including the stop codon.

1 M K L W I H L F Y S S L L
1 t c g g a t t t c a t c a c a t g a c a a c A T G A A G C T G T G G A T T C A T C T C T T T T A T T C A T C T C T C C T
14 A C I S L H S Q T P V L S S R G S C D S
61 T G C C T G T A T A T C T T T A C A C T C C C A A A C T C C A G T G C T C T C A T C C A G A G G C T C T T G T G A T T C
34 L C N C E E K D G T M L I N C E A K G I
121 T C T T T G C A A T T G T G A G G A A A A G A T G G C A C A A T G C T A A T A A A T T G T G A A G C A A A A G G T A T
54 K M V S E I S V P P S R P F Q L S L L N
181 C A A G A T G G T A T C T G A A A T A A G T G T G C C A C C A T C A C G A C C T T T C C A A C T A A G C T T A T T A A A
74 N G L T M L H T N D F S G L T N A I S I
241 T A A C G G C T T G A C G A T G C T T C A C A C A A A T G A C T T T T C T G G G C T T A C C A A T G C T A T T T C A A T
94 H L G F N N I A D I E I G A F N G L G L
301 A C A C C T T G G A T T T A A C A A T A T T G C A G A T A T T G A G A T A G G T G C A T T T A A T G G C C T T G G C C T
114 L K Q L H I N H N S L E I L K E D T F H
361 C C T G A A C A A C T T C A T A T C A A T C A C A A T T C T T T A G A A A T T C T T A A G A G G A T A C T T T C C A
134 G L E N L E F L Q A D N N F I T V I E P
421 T G G A C T G G A A A C C T G G A A T T C C T G C A A G C A G A T A A C A A T T T T A T C A C A G T G A T T G A A C C
154 S A F S K L N R L K V L I L N D N A I E
481 A A G T G C C T T T A G C A A G C T C A A C A G A C T C A A A G T G T T A A T T T T A A T G A C A A T G C T A T T G A
174 S L P P N I F R F V P L T H L D L R G N
541 G A G T C T T C C T C C A A C A T C T T C C G A T T T G T T C C T T T A A C C C A T C T A G A T C T T C G T G G A A A
194 Q L Q T L P Y V G F L E H I G R I L D L
601 T C A A T T A C A A C A T T G C C T T A T G T T G G T T T T C T C G A A C A C A T T G G C C G A A T A T T G G A T C T
214 Q L E D N K W A C N C D L L Q L K T W L
661 T C A G T T G G A G G A C A C A A A T G G G C C T G C A A T T G T G A C T T A T T G C A G T T A A A A C T T G G T T
234 E N M P P Q S I I G D V V C N S P P F F
721 G G A G A A C A T G C C T C C A G A G T C T A T A A T T G G T G A T G T T G T C T G C A A C A G C C C T C C A T T T T T
254 K G S I L S R L K K E S I C P T P P V Y
781 T A A G G A A G T A T A C T C A G T A G A C T A A A G A A G G A A T C T A T T T G C C C T A C T C C A C C A G T G T A
274 E E H E D P S G S L H L A A T S S I N D
841 T G A A G A C A T G A G G A T C C T T C A G G A T C A T T A C A T C T G G C A G C A A C A T C T T C A A T A A A T G A

294 S R M S T K T T S I L K L P T K A P G L
901 TAGTCGCATGTCAACTAAGACCACGTCCATTCTAAAACTACCCACCAAAGCACCAGGTTT
314 I P Y I T K P S T Q L P G P Y C P I P C
961 GATACCTTATATTACAAAGCCATCCACTCAACTTCCAGGACCTTACTGCCCTATTTCCTTG
334 N C K V L S P S G L L I H C Q E R N I E
1021 TAAC TGCAAAGTCCTATCCCCATCAGGACTTCTAATACATTGTCAGGAGCGCAACATTGA
354 S L S D L R P P P Q N P R K L I L A G N
1081 AAGCTTATCAGATCTGAGACCTCCTCCGCAAAATCCTAGAAAGCTCATTCTAGCGGGAAA
374 I I H S L M K S D L V E Y F T L E M L H
1141 TATTATTACAGTTTAAATGAAGTCTGATCTAGTGAATATTTCACTTTGGAAATGCTTCA
394 L G N N R I E V L E E G S F M N L T R L
1201 CTTGGGAAACAATCGTATTGAAGTTCTTGAAGAAGGATCGTTTATGAACCTAACGAGATT
414 Q K L Y L N G N H L T K L S K G M F L G
1261 ACAAAAACCTCTATCTAAATGGTAACCACCTGACCAAATTAAGTAAAGGCATGTTCTCTTG
434 L H N L E Y L Y L E Y N A I K E I L P G
1321 TCTCCATAATCTTGAATACTTATATCTTGAATACAATGCCATTAAGGAAATACTGCCAGG
454 T F N P M P K L K V L Y L N N N L L Q V
1381 AACCTTTAATCCAATGCCTAAACTTAAAGTCTGTATTTAAATAACAACCTCCTCCAAGT
474 L P P H I F S G V P L T K V N L K T N Q
1441 TTTACCACCACATATTTTTTCAGGGGTTCTCTAACTAAGGTAAATCTTAAACAAACCA
494 F T H L P V S N I L D D L D L L T Q I D
1501 GTTTACCCATCTACCTGTAAGTAATATTTTGATGATCTTGATTGCTAACCCAGATTGA
514 L E D N P W D C S C D L V G L Q Q W I Q
1561 CCTTGAGGATAACCCCTGGGACTGCTCCTGTGACCTGGTTGGACTGCAGCAATGGATACA
534 K L S K N T V T D D I L C T S P G H L D
1621 AAAGTTAAGCAAGAACACAGTGACAGATGACATCCTCTGCACTTCCCCCGGCATCTCGA
554 K K E L K A L N S E I L C P G L V N N P
1681 CAAAAGGAATTGAAAGCCCTAAATAGTGAAATTCTCTGTCCAGGTTTAGTAAATAACCC
574 S M P T Q T S Y L M V T T P A T T T N T
1741 ATCCATGCCAACACAGACTAGTTACCTTATGGTCACCACTCCTGCAACAACAACAATAC
594 A D T I L R S L T D A V P L S V L I L G
1801 GGCTGATACTATTTTACGATCTCTTACGGACGCTGTGCCACTGTCTGTTCTAATATTGGG
614 L L I M F I T I V F C A A G I V V L V L
1861 ACTTCTGATTATGTTTCATCACTATTGTTTTCTGTGCTGCAGGGATAGTGGTTCTTGTTC
634 H R R R R Y K K K Q V D E Q M R D N S P
1921 TCACCGCAGGAGAAGATACAAAAGAAACAAGTAGATGAGCAAATGAGAGACAACAGTCC
654 V H L Q Y S M Y G H K T T H H T T E R P
1981 TGTGCATCTTCAGTACAGCATGTATGGCCATAAAACCACTCATCACTACTGAAAGACC
674 S A S L Y E Q H M V S P M V H V Y R S P
2041 CTCTGCCTCACTCTATGAACAGCACATGGTGAGCCCCATGGTTCATGTCTATAGAAGTCC
694 S F G P K H L E E E E E R N E K E G S D
2101 ATCCTTTGGTCCAAAGCATCTGGAAGAGGAAGAAGAGAGGAATGAGAAAGAAGGAAGTGA

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714  A K H L Q R S L L E Q E N H S P L T G S
2161 TGCAAAACATCTCCAAAGAAGTCTTTTGAACAGGAAAATCATTACCACTCACAGGGTC
734  N M K Y K T T N Q S T E F L S F Q D A S
2221 AAATATGAAATACAAAACCACGAACCAATCAACAGAATTTTTATCCTTCCAAGATGCCAG
754  S L Y R N I L E K E R E L Q Q L G I T E
2281 CTCATTGTACAGAAACATTTTAGAAAAAGAAAGGGAAGTTCAGCAACTGGGAATCACAGA
774  Y L R K N I A Q L Q P D M E A H Y P G A
2341 ATACCTAAGGAAAAACATTGCTCAGCTCCAGCCTGATATGGAGGCACATTATCCTGGAGC
794  H E E L K L M E T L M Y S R P R K V L V
2401 CCACGAAGAGCTGAAGTTAATGGAAACATTAATGTACTCACGTCCAAGGAAGGTATTAGT
814  E Q T K N E Y F E L K A N L H A E P D Y
2461 GGAACAGACAAAAAATGAGTATTTTGAAGCTTAAAGCTAATTTACATGCTGAACCTGACTA
834  L E V L E Q Q T *
2521 TTTAGAAGTCCTGGAGCAGCAAACATAGatggaga

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Figure 2C. The cDNA (SEQ ID NO: 6) and amino acid sequence (SEQ ID NO: 7) of 158P1D7 v.3.
The start methionine is underlined. The open reading frame extends from nucleic acid 23-2221 including the stop codon.

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1          M K L W I H L F Y S S L L
1  tcggatttcatcacatgacaacATGAAGCTGTGGATTCATCTCTTTTATTCATCTCTCCT
14  A C I S L H S Q T P V L S S R G S C D S
61  TGCCTGTATATCTTTACACTCCCAAACCTCCAGTGCTCTCATCCAGAGGCTCTTGTGATTC
34  L C N C E E K D G T M L I N C E A K G I
121 TCTTTGCAATTGTGAGGAAAAAGATGGCACAATGCTAATAAATTGTGAAGCAAAAGGTAT
54  K M V S E I S V P P S R P F Q L S L L N
181 CAAGATGGTATCTGAAATAAGTGTGCCACCATCACGACCTTTCCAACCTAAGCTTATTAAA
74  N G L T M L H T N D F S G L T N A I S I
241 TAACGGCTTGACGATGCTTCACACAAATGACTTTTCTGGGCTTACCAATGCTATTTCAAT
94  H L G F N N I A D I E I G A F N G L G L
301 ACACCTTGGATTTAACAATATTGCAGATATTGAGATAGGTGCATTTAATGGCCTTGGCCT
114 L K Q L H I N H N S L E I L K E D T F H
361 CCTGAAACAACTTCATATCAATCACAATTCTTTAGAAATTCTTAAAGAGGATACTTTCCA
134 G L E N L E F L Q A D N N F I T V I E P
421 TGGACTGGAAAACCTGGAATTCCTGCAAGCAGATAACAATTTTATCACAGTGATTGAACC
154 S A F S K L N R L K V L I L N D N A I E
481 AAGTGCCTTTAGCAAGCTCAACAGACTCAAAGTGTTAATTTTAAATGACAATGCTATTGA
174 S L P P N I F R F V P L T H L D L R G N
541 GAGTCTTCCTCCAAACATCTTCCGATTTGTTCTTTAACCCATCTAGATCTTCGTGGAAA
194 Q L Q T L P Y V G F L E H I G R I L D L
601 TCAATTACAAACATTGCCTTATGTTGGTTTCTCGAACACATTGGCCGAATATTGGATCT
214 Q L E D N K W A C N C D L L Q L K T W L

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661 TCAGTTGGAGGACAACAAATGGGCCTGCAATTGTGACTTATTGCAGTTAAAACTTGGTT
234 E N M P P Q S I I G D V V C N S P P F F
721 GGAGAACATGCCTCCACAGTCTATAATTGGTGATGTTGTCTGCAACAGCCCTCCATTTTT
254 K G S I L S R L K K E S I C P T P P V Y
781 TAAAGGAAGTATACTCAGTAGACTAAAGAAGGAATCTATTTGCCCTACTCCACCAGTGTA
274 E E H E D P S G S L H L A A T S S I N D
841 TGAAGACATGAGGATCCTTCAGGATCATTACATCTGGCAGCAACATCTTCAATAAATGA
294 S R M S T K T T S I L K L P T K A P G L
901 TAGTCGCATGTCAACTAAGACCACGTCCATTCTAAAACTACCCACCAAAGCACCAGTTT
314 I P Y I T K P S T Q L P G P Y C P I P C
961 GATACCTTATATTACAAAGCCATCCACTCAACTTCCAGGACCTTACTGCCCTATTTCCTTG
334 N C K V L S P S G L L I H C Q E R N I E
1021 TAACTGCAAAGTCCTATCCCCATCAGGACTTCTAATACATTGTGAGGAGCGCAACATTGA
354 S L S D L R P P P Q N P R K L I L A G N
1081 AAGCTTATCAGATCTGAGACCTCCTCCGAAAATCCTAGAAAGCTCATTCTAGCGGGAAA
374 I I H S L M K S D L V E Y F T L E M L H
1141 TATTATTCACAGTTTAATGAAGTCTGATCTAGTGGAATATTTCACTTTGGAAATGCTTCA
394 L G N N R I E V L E E G S F M N L T R L
1201 CTTGGGAAACAATCGTATTGAAGTTCTTGAAGAAGGATCGTTTATGAACCTAACGAGATT
414 Q K L Y L N G N H L T K L S K G M F L G
1261 ACAAAAACCTCTATCTAAATGGTAACCACCTGACCAAATTAAGTAAAGGCATGTTCTCTGG
434 L H N L E Y L Y L E Y N A I K E I L P G
1321 TCTCCATAATCTTGAATACTTATATCTTGAATACAATGCCATTAAGGAAATACTGCCAGG
454 T F N P M P K L K V L Y L N N N L L Q V
1381 AACCTTTAATCCAATGCCTAAACTTAAAGTCCTGTATTTAAATAACAACCTCCTCCAAGT
474 L P P H I F S G V P L T K V N L K T N Q
1441 TTTACCACCACATATTTTTTTCAGGGGTTCTCTAACTAAGGTAAATCTTAAAACAAACCA
494 F T H L P V S N I L D D L D L L T Q I D
1501 GTTTACCCATCTACCTGTAAGTAATATTTTGGATGATCTTGATTTACTAACCAGATTGA
514 L E D N P W D C S C D L V G L Q Q W I Q
1561 CCTTGAGGATAACCCCTGGGACTGCTCCTGTGACCTGGTTGGACTGCAGCAATGGATACA
534 K L S K N T V T D D I L C T S P G H L D
1621 AAAGTTAAGCAAGAACACAGTGACAGATGACATCCTCTGCACCTCCCCGGGCATCTCGA
554 K K E L K A L N S E I L C P G L V N N P
1681 CAAAAAGGAATTGAAAGCCCTAAATAGTGAAATTCTCTGTCCAGGTTTAGTAAATAACCC
574 S M P T Q T S Y L M V T T P A T T T N T
1741 ATCCATGCCAACACAGACTAGTTACCTTATGGTCACCACTCCTGCAACAACAACAAATAC
594 A D T I L R S L T D A V P L S V L I L G
1801 GGCTGATACTATTTTACGATCTCTTACGGACGCTGTGCCACTGTCTGTTCTAATATTGGG
614 L L I M F I T I V F C A A G I V V L V L
1861 ACTTCTGATTATGTTTCATCACTATTGTTTTCTGTGCTGCAGGGATAGTGGTTCTTGTCT
634 H R R R R Y K K K Q V D E Q M R D N S P

1921 TCACCGCAGGAGAAGATACAAAAAGAAACAAGTAGATGAGCAAATGAGAGACAACAGTCC
654 V H L Q Y S M Y G H K T T H H T T E R P
1981 TGTGCATCTTCAGTACAGCATGTATGGCCATAAAACCACTCATCACACTACTGAAAGACC
674 S A S L Y E Q H M G A H E E L K L M E T
2041 CTCTGCCTCACTCTATGAACAGCACATGGGAGCCCACGAAGAGCTGAAGTTAATGGAAAC
694 L M Y S R P R K V L V E Q T K N E Y F E
2101 ATTAATGTACTCAGTCCAAGGAAGGTATTAGTGGAACAGACAAAAATGAGTATTTTGA
714 L K A N L H A E P D Y L E V L E Q Q T *
2161 ACTTAAAGCTAATTTACATGCTGAACCTGACTATTTAGAAAGTCTCTGGAGCAGCAAACATA
2221 Gatggaga

Figure 2D. The cDNA (SEQ ID NO: 8) and amino acid sequence (SEQ ID NO: 9) of 158P1D7 v.4.
The start methionine is underlined. The open reading frame extends from nucleic acid 23-1210 including the stop codon.

1 M K L W I H L F Y S S L L
1 tcggatttcatcacatgacaacATGAAGCTGTGGATTTCATCTCTTTTATTCATCTCTCCT
14 A C I S L H S Q T P V L S S R G S C D S
61 TGCCTGTATATCTTTACTCCAACTCCAGTGCTCTCATCCAGAGGCTCTTGTGATTCC
34 L C N C E E K D G T M L I N C E A K G I
121 TCTTTGCAATTGTGAGGAAAAAGATGGCACAATGCTAATAAATTGTGAAGCAAAAGGTAT
54 K M V S E I S V P P S R P F Q L S L L N
181 CAAGATGGTATCTGAAATAAGTGTGCCACCATCACGACCTTTCCAACTAAGCTTATTAA
74 N G L T M L H T N D F S G L T N A I S I
241 TAACGGCTTGACGATGCTTCACACAAATGACTTTTCTGGGCTTACCAATGCTATTTCAAT
94 H L G F N N I A D I E I G A F N G L G L
301 ACACCTTGGATTTAACAATATTGCAGATATTGAGATAGGTGCATTTAATGGCCTTGGCCT
114 L K Q L H I N H N S L E I L K E D T F H
361 CCTGAAACAACTTCATATCAATCACAATTCTTTAGAAATTCTTAAAGAGGATACTTTCCA
134 G L E N L E F L Q A D N N F I T V I E P
421 TGGACTGGAAAACCTGGAATTCCTGCAAGCAGATAACAATTTTATCACAGTGATTGAACC
154 S A F S K L N R L K V L I L N D N A I E
481 AAGTGCCTTTAGCAAGCTCAACAGACTCAAAGTGTTAATTTTAAATGACAATGCTATTGA
174 S L P P N I F R F V P L T H L D L R G N
541 GAGTCTTCCTCCAAACATCTTCCGATTGTTCCTTTAACCCATCTAGATCTTCGTGGAAA
194 Q L Q T L P Y V G F L E H I G R I L D L
601 TCAATTACAAACATTGCCTTATGTTGGTTTCTCGAACACATTGGCCGAATATTGGATCT
214 Q L E D N K W A C N C D L L Q L K T W L
661 TCAGTTGGAGGACAACAAATGGGCCTGCAATTGTGACTTATTGCAGTTAAAACTTGGTT
234 E N M P P Q S I I G D V V C N S P P F F
721 GGAGAACATGCCTCCACAGTCTATAATTGGTGATGTTGTCTGCAACAGCCCTCCATTTT
254 K G S I L S R L K K E S I C P T P P V Y

```

781 TAAAGGAAGTATACTCAGTAGACTAAAGAAGGAATCTATTTGCCCTACTCCACCAGTGTA
274 E E H E D P S G S L H L A A T S S I N D
841 TGAAGAACATGAGGATCCTTCAGGATCATTACATCTGGCAGCAACATCTTCAATAAATGA
294 S R M S T K T T S I L K L P T K A P G L
901 TAGTCGCATGTCAACTAAGACCACGTCCATTCTAAAACTACCCACCAAAGCACCAGGTTT
314 I P Y I T K P S T Q L P G P Y C P I P C
961 GATACCTTATATTACAAAGCCATCCACTCAACTTCCAGGACCTTACTGCCCTATTCTTGG
334 N C K V L S P S G L L I H C Q E R N I E
1021 TAACTGCAAAGTCTATCCCCATCAGGACTTCTAATACATTGTCAGGAGCGCAACATTGA
354 S L S D L R P P P Q N P R K L I L A G N
1081 AAGCTTATCAGATCTGAGACCTCCTCCGCAAAATCCTAGAAAGCTCATTCTAGCGGGAAA
374 I I H S L M K S I L W S K A S G R G R R
1141 TATTATTCACAGTTTAATGAAGTCCATCCTTTGGTCCAAAGCATCTGGAAGAGGAAGAAG
394 E E *
1201 AGAGGAATGAgaaagaaggaagtgatgcaaaacatctccaaagaagtcttttggaaacagg
1261 aaaatcattcaccactcacagggtcaaatatgaaatacaaaaccacgaaccaatcaacag
1321 aatttttatccttccaagatgccagctcattgtacagaaacattttagaaaaagaaaggg
1381 aacttcagcaactgggaatcacagaatacctaaggaaaaacattgctcagctccagcctg
1441 atatggaggcacattatcctggagcccacgaagagctgaagttaatggaaacattaatgt
1501 actcacgtccaaggaaggtattagtggaacagacaaaaaatgagtattttgaacttaaag
1561 ctaatttacatgctgaacctgactatttagaagtcctggagcagcaaacatagatggaga

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Figure 2E. The cDNA (SEQ ID NO: 10) and amino acid sequence (SEQ ID NO: 11) of 158P1D7 v.5.
The start methionine is underlined. The open reading frame extends from nucleic acid 480-3005 including the stop codon.

```

1 gcgtcgacaacaagaaatactagaaaaggaggaaggagaacattgctgcagcttggatct
61 acaacctaagaaagcaagagtgatcaatctcagctctgttaaacatcttgtttacttact
121 gcattcagcagcttgcaaattgggttaactatatgcaaaaaagtgcagcatagctgtgaagta
181 tgccgtgaatttttaattgagggaaaaaggacaattgcttcaggatgctctagtatgcact
241 ctgcttgaaatattttcaatgaaatgctcagttattctatctttgaccagagggttttaact
301 ttatgaagctatgggacttgacaaaaagtgatatttgagaagaaagtacgcagtggttgg
361 tgttttcttttttttaataaaggaattgaattactttgaacacctcttccagctgtgcatt
1 M
421 tacagataacgtcaggaagagtcctctgctttacagaatcggatttcacatgacaacA
2 K L W I H L F Y S S L L A C I S L H S Q
481 TGAAGCTGTGGATTCATCTCTTTTATTCATCTCTCCTTGCCTGTATATCTTTACTACTCCC
22 T P V L S S R G S C D S L C N C E E K D
541 AAAGCTCCAGTGTCTCATCCAGAGGCTCTTGTGATTCTCTTTGCAATTGTGAGGAAAAAG
42 G T M L I N C E A K G I K M V S E I S V
601 ATGGCACAATGCTAATAAATTGTGAAGCAAAAGGTATCAAGATGGTATCTGAAATAAGTG
62 P P S R P F Q L S L L N N G L T M L H T

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661 TGCCACCATCACGACCTTTCCAACCTAAGCTTATTAAATAACGGCTTGACGATGCTTCACA
82 N D F S G L T N A I S I H L G F N N I A
721 CAAATGACTTTTCTGGGCTTACCAATGCTATTTCAATACACCTTGGATTAAACAATATTG
102 D I E I G A F N G L G L L K Q L H I N H
781 CAGATATTGAGATAGGTGCATTTAATGGCCTTGGCCTCCTGAAACAACTTCATATCAATC
122 N S L E I L K E D T F H G L E N L E F L
841 ACAATTCTTTAGAAATTCTTAAAGAGGATACTTTCCATGGACTGGAAAACCTGGAATTCC
142 Q A D N N F I T V I E P S A F S K L N R
901 TGCAAGCAGATAACAATTTTATCACAGTGATTGAACCAAGTGCCTTTAGCAAGCTCAACA
162 L K V L I L N D N A I E S L P P N I F R
961 GACTCAAAGTGTTAATTTTAAATGACAATGCTATTGAGAGTCTTCTCCAAACATCTTCC
182 F V P L T H L D L R G N Q L Q T L P Y V
1021 GATTTGTTCTTTAACCCATCTAGATCTTCGTGGAAATCAATTACAAACATTGCCTTATG
202 G F L E H I G R I L D L Q L E D N K W A
1081 TTGGTTTTCTCGAACACATTGGCCGAATATTGGATCTTCAGTTGGAGGACAACAAATGGG
222 C N C D L L Q L K T W L E N M P P Q S I
1141 CCTGCAATTGTGACTTATTGCAGTTAAAACTTGGTTGGAGAACATGCCTCCACAGTCTA
242 I G D V V C N S P P F F K G S I L S R L
1201 TAATTGGTGATGTTGTCTGCAACAGCCCTCCATTTTTTAAAGGAAGTATACTCAGTAGAC
262 K K E S I C P T P P V Y E E H E D P S G
1261 TAAAGAAGGAATCTATTTGCCCTACTCCACCAGTGTATGAAGAACATGAGGATCCTTCAG
282 S L H L A A T S S I N D S R M S T K T T
1321 GATCATTACATCTGGCAGCAACATCTTCAATAAATGATAGTCGCATGTCAACTAAGACCA
302 S I L K L P T K A P G L I P Y I T K P S
1381 CGTCCATTCTAAAACTACCCACCAAAGCACCAGGTTTGATACCTTATATTACAAAGCCAT
322 T Q L P G P Y C P I P C N C K V L S P S
1441 CCACTCAACTCCAGGACCTTACTGCCCTATTCCTTGTAAGTCAAAGTCTATCCCCAT
342 G L L I H C Q E R N I E S L S D L R P P
1501 CAGGACTTCTAATACATTGTGAGGAGCGCAACATTGAAAGCTTATCAGATCTGAGACCTC
362 P Q N P R K L I L A G N I I H S L M K S
1561 CTCCGCAAAATCCTAGAAAGCTCATTCTAGCGGAAATATTATTACAGTTTAAATGAAGT
382 D L V E Y F T L E M L H L G N N R I E V
1621 CTGATCTAGTGAATATTTCACTTTGGAAATGCTTCACTTGGGAAACAATCGTATTGAAG
402 L E E G S F M N L T R L Q K L Y L N G N
1681 TTCTTGAAGAAGGATCGTTTATGAACCTAACGAGATTACAAAACTCTATCTAAATGGTA
422 H L T K L S K G M F L G L H N L E Y L Y
1741 ACCACCTGACCAAATTAAGTAAAGGCATGTTCTTGGTCTCCATAATCTTGAATACTTAT
442 L E Y N A I K E I L P G T F N P M P K L
1801 ATCTTGAATACAATGCCATTAAGGAAATACTGCCAGGAACCTTTAATCCAATGCCTAAAC
462 K V L Y L N N N L L Q V L P P H I F S G
1861 TTAAAGTCCTGTATTTAAATAACAACCTCCTCCAAGTTTTACCACCACATATTTTTTTCAG
482 V P L T K V N L K T N Q F T H L P V S N

1921 GGGTTCCTCTAACTAAGGTAAATCTTAAAAACAAACCAGTTTACCCATCTACCTGTAAGTA
502 I L D D L D L L T Q I D L E D N P W D C
1981 ATATTTTGGATGATCTTGATTTACTAACCAGATTGACCTTGAGGATAACCCCTGGGACT
522 S C D L V G L Q Q W I Q K L S K N T V T
2041 GCTCCTGTGACCTGGTTGGACTGCAGCAATGGATACAAAAGTTAAGCAAGAACACAGTGA
542 D D I L C T S P G H L D K K E L K A L N
2101 CAGATGACATCCTCTGCACCTCCCCCGGGCATCTCGACAAAAAGGAATTGAAAGCCCTAA
562 S E I L C P G L V N N P S M P T Q T S Y
2161 ATAGTGAAATTCTCTGTCCAGGTTTAGTAAATAACCCATCCATGCCAACACAGACTAGTT
582 L M V T T P A T T T N T A D T I L R S L
2221 ACCTTATGGTCACTCCTGCAACAACAACAAATACGGCTGATACTATTTTACGATCTC
602 T D A V P L S V L I L G L L I M F I T I
2281 TTACGGACGCTGTGCCACTGTCTGTTCTAATATTGGGACTTCTGATTATGTTTCATCACTA
622 V F C A A G I V V L V L H R R R R Y K K
2341 TTGTTTTCTGTGCTGCAGGGATAGTGGTTCTTGTTCCTTACCAGCAGGAGAAGATACAAA
642 K Q V D E Q M R D N S P V H L Q Y S M Y
2401 AGAAACAAGTAGATGAGCAAATGAGAGACAACAGTCCTGTGCATCTTCAGTACAGCATGT
662 G H K T T H H T T E R P S A S L Y E Q H
2461 ATGGCCATAAAACCACTCATCACACTACTGAAAGACCCTCTGCCTCACTCTATGAACAGC
682 M V S P M V H V Y R S P S F G P K H L E
2521 ACATGGTGAGCCCCATGGTTCATGTCTATAGAAGTCCATCCTTGGTCCAAAGCATCTGG
702 E E E E R N E K E G S D A K H L Q R S L
2581 AAGAGGAAGAAGAGAGGAATGAGAAAGAAGGAAGTGATGCAAAACATCTCCAAAGAAGTC
722 L E Q E N H S P L T G S N M K Y K T T N
2641 TTTTGGAACAGGAAAATCATTCACTCAGGGTCAAATATGAAATACAAAACCACGA
742 Q S T E F L S F Q D A S S L Y R N I L E
2701 ACCAATCAACAGAATTTTTATCCTTCCAAGATGCCAGCTCATTGTACAGAAACATTTTAG
762 K E R E L Q Q L G I T E Y L R K N I A Q
2761 AAAAAGAAAGGGAAGTTTCACTGCACTGGGAATCACAGAATACCTAAGGAAAAACATTGCTC
782 L Q P D M E A H Y P G A H E E L K L M E
2821 AGCTCCAGCTGATATGGAGGCACATTATCCTGGAGCCCACGAAGAGCTGAAGTTAATGG
802 T L M Y S R P R K V L V E Q T K N E Y F
2881 AAACATTAATGTACTCACGTCCAAGGAAGGTATTAGTGGAACAGACAAAAATGAGTATT
822 E L K A N L H A E P D Y L E V L E Q Q T
2941 TTGAACTTAAAGCTAATTTACATGCTGAACCTGACTATTTAGAAGTCCTGGAGCAGCAAA
842 *
3001 CATAGatggagaggttgagggctttcgccagaaatgctgtgattctgttattaagtccata
3061 ccttgtaaataagtgaccttacgtgagtggtcatcaatcagaacctaacacagagtaaa
3121 ctatggggaaaaaaaagaagacgaaacagaaactcagggatcactgggagaagccatgg
3181 cataatcttcaggcaattagtctgtccaaataaacatacatccttggcatgtaaatca
3241 tcaagggtaatagtaatatcatatacctgaaacgtgtctcataggagtcctctctgcac

Figure 2F. The cDNA (SEQ ID NO: 12) and amino acid sequence (SEQ ID NO: 13) of 158P1D7 v.6.

The start methionine is underlined. The open reading frame extends from nucleic acid 23-1612 including the stop codon.

```

1           M K L W I H L F Y S S L L
1  tcggatttcacatgacaacATGAAGCTGTGGATTCATCTCTTTTATTCATCTCTCCT
14  A C I S L H S Q T P V L S S R G S C D S
61  TGCCTGTATATCTTTACTCCAACTCCAGTGCTCTCATCCAGAGGCTCTTGATTC
34  L C N C E E K D G T M L I N C E A K G I
121 TCTTTGCAATTGTGAGGAAAAAGATGGCACAATGCTAATAAATTGTGAAGCAAAAGGTAT
54  K M V S E I S V P P S R P F Q L S L L N
181 CAAGATGGTATCTGAAATAAGTGTGCCACCATCACGACCTTTCCAATAAGCTTATTAA
74  N G L T M L H T N D F S G L T N A I S I
241 TAACGGCTTGACGATGCTTCACACAAATGACTTTTCTGGGCTTACCAATGCTATTTCAT
94  H L G F N N I A D I E I G A F N G L G L
301 ACACCTTGGATTTAACAATATTGCAGATATTGAGATAGGTGCATTAAATGGCCTTGGCCT
114 L K Q L H I N H N S L E I L K E D T F H
361 CCTGAAACAACTTCATATCAATCACAATCTTTAGAAATCTTAAAGAGGATACTTTCCA
134 G L E N L E F L Q A D N N F I T V I E P
421 TGGACTGGAAAACCTGGAATTCCTGCAAGCAGATAACAATTTTATCACAGTGATTGAACC
154 S A F S K L N R L K V L I L N D N A I E
481 AAGTGCCTTTAGCAAGCTCAACAGACTCAAAGTGTTAATTTTAAATGACAATGCTATTGA
174 S L P P N I F R F V P L T H L D L R G N
541 GAGTCTTCCTCCAAACATCTTCCGATTGTTCCTTTAACCCATCTAGATCTTCGTGGAAA
194 Q L Q T L P Y V G F L E H I G R I L D L
601 TCAATTACAAACATTGCCTTATGTTGGTTTCTCGAACACATTGGCCGAATATTGGATCT
214 Q L E D N K W A C N C D L L Q L K T W L
661 TCAGTTGGAGGACAACAAATGGGCCTGCAATTGTGACTTATTGCAGTTAAAACTTGGTT
234 E N M P P Q S I I G D V V C N S P P F F
721 GGAGAATGCCTCCACAGTCTATAATTGGTGATGTTGTCTGCAACAGCCCTCCATTTT
254 K G S I L S R L K K E S I C P T P P V Y
781 TAAAGGAAGTATACTCAGTAGACTAAAGAAGGAATCTATTTGCCCTACTCCACCAGTGTA
274 E E H E D P S G S L H L A A T S S I N D
841 TGAAGAACATGAGGATCCTTCAGGATCATTACATCTGGCAGCAACATCTTCAATAAATGA
294 S R M S T K T T S I L K L P T K A P G L
901 TAGTCGCATGTCAACTAAGACCAGTCCATTCTAAACTACCCACCAAAGCACCAGGTTT
314 I P Y I T K P S T Q L P G P Y C P I P C
961 GATACCTTATATTACAAAGCCATCCACTCAACTTCCAGGACCTTACTGCCCTATTCTTG
334 N C K V L S P S G L L I H C Q E R N I E
1021 TAACTGCAAAGTCTATCCCCATCAGGACTTCTAATACATTGTGAGGAGCGCAACATTGA
354 S L S D L R P P P Q N P R K L I L A G N
1081 AAGCTTATCAGATCTGAGACCTCCTCCGAAAATCCTAGAAAGCTCATTCTAGCGGGAAA

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374 I I H S L M N P S F G P K H L E E E E E
1141 TATTATTACAGTTTAAATGAATCCATCCTTTGGTCCAAAGCATCTGGAAGAGGAAGAAGA
394 R N E K E G S D A K H L Q R S L L E Q E
1201 GAGGAATGAGAAAGAAGGAAGTGATGCAAAACATCTCCAAAGAAGTCTTTTGGAACAGGA
414 N H S P L T G S N M K Y K T T N Q S T E
1261 AAATCATTCACCACTCACAGGGTCAAATATGAAATACAAAACCACGAACCAATCAACAGA
434 F L S F Q D A S S L Y R N I L E K E R E
1321 ATTTTATCCTTCCAAGATGCCAGCTCATTGTACAGAAACATTTTAGAAAAAGAAAGGGA
454 L Q Q L G I T E Y L R K N I A Q L Q P D
1381 ACTTCAGCAACTGGGAATCACAGAATACCTAAGGAAAAACATTGCTCAGCTCCAGCCTGA
474 M E A H Y P G A H E E L K L M E T L M Y
1441 TATGGAGGCACATTATCCTGGAGCCCACGAAGAGCTGAAGTTAATGGAAACATTAATGTA
494 S R P R K V L V E Q T K N E Y F E L K A
1501 CTCACGTCCAAGGAAGGTATTAGTGGAAACAGACAAAAAATGAGTATTTGAACTTAAAGC
514 N L H A E P D Y L E V L E Q Q T *
1561 TAATTTACATGCTGAACCTGACTATTTAGAAGTCCTGGAGCAGCAAACATAGatggaga

Figure 3:

Figure 3A. Amino acid sequence 158P1D7 v.1 (SEQ ID NO: 14). The 158P1D7 v.1 protein has 841 amino acids.

```

1 MKLWIHLFYS SLLACISLHS QTPVLSSRGs CDSLNCNEEK DGTMLINCEA KGIKMVSEIS
61 VPPSRPFQLS LLNNGLTMLH TNDFSGLTNA ISIH LGFN NI ADIEIGAFNG LGLLKQLHIN
121 HNSLEILKED TFHGLENLEF LQADNNFITV IEPsAFsKLN RLKVLILNDN AIESLPPNIF
181 RFVPLTHLDL RGNQLQTLPY VGFLEHIGRI LDLQLEDNKW ACNCDLLQLK TWLENMPPQS
241 IIGDVVCNSP PFFKGSILSR LKKESICPTP PVYEEHEDPS GSLHLAATSS INDSRMSTKT
301 TSILKLPTKA PGLIPYITKP STQLPGPYCP IPCNCKVLSP SGLLIHCQER NIESLSDLRP
361 PPQNPRKLIL AGNIIHSLMK SDLVEYFTLE MLHLGNNRIE VLEEGsFMNL TRLQKLYLNG
421 NHLTKLSKGM FLGLHNLEYL YLEYNAIKEI LPGTFNMPK LKVLYLNNNL LQVLPPHIFS
481 GVPLTKVNLK TNQFTHLPVS NILDDL DLT QIDLEDNPWD CSCDLVGLQQ WIQKLSKNTV
541 TDDILCTSPG HLDKKELKAL NSEILCPGLV NNPSMPTQTS YLMVTT PATT TNTADTILRS
601 LTDAVPLSVL ILGLLIMFIT IVFCAAGIVV LVLHRRRRYK KKQVDEQMRD NSPVLHLQYSM
661 YGHKTTHHTT ERPSASLYEQ H MVSPMVHVY RSPSFGPKHL EEEEEERNEKE GSDAKHLQRS
721 LLEQENHSPL TGSNMKYKTT NQSTEF LSFQ DASSLYRNIL EKERELQQLG ITEYLRKNIA
781 QLQPDMEAHY PGAHEELKLM ETLMSRPRK VLVEQTKNEY FELKANLHAE PDYLEVLEQQ
841 T

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Figure 3B. Amino acid sequence 158P1D7 v.3 (SEQ ID NO: 15). The 158P1D7 v.3 protein has 732 amino acids.

```

1 MKLWIHLFYS SLLACISLHS QTPVLSSRGs CDSLNCNEEK DGTMLINCEA KGIKMVSEIS
61 VPPSRPFQLS LLNNGLTMLH TNDFSGLTNA ISIH LGFN NI ADIEIGAFNG LGLLKQLHIN
121 HNSLEILKED TFHGLENLEF LQADNNFITV IEPsAFsKLN RLKVLILNDN AIESLPPNIF
181 RFVPLTHLDL RGNQLQTLPY VGFLEHIGRI LDLQLEDNKW ACNCDLLQLK TWLENMPPQS
241 IIGDVVCNSP PFFKGSILSR LKKESICPTP PVYEEHEDPS GSLHLAATSS INDSRMSTKT
301 TSILKLPTKA PGLIPYITKP STQLPGPYCP IPCNCKVLSP SGLLIHCQER NIESLSDLRP
361 PPQNPRKLIL AGNIIHSLMK SDLVEYFTLE MLHLGNNRIE VLEEGsFMNL TRLQKLYLNG
421 NHLTKLSKGM FLGLHNLEYL YLEYNAIKEI LPGTFNMPK LKVLYLNNNL LQVLPPHIFS
481 GVPLTKVNLK TNQFTHLPVS NILDDL DLT QIDLEDNPWD CSCDLVGLQQ WIQKLSKNTV
541 TDDILCTSPG HLDKKELKAL NSEILCPGLV NNPSMPTQTS YLMVTT PATT TNTADTILRS
601 LTDAVPLSVL ILGLLIMFIT IVFCAAGIVV LVLHRRRRYK KKQVDEQMRD NSPVLHLQYSM
661 YGHKTTHHTT ERPSASLYEQ H MGAHEELKL METLMSRPR KVLVEQTKNE YFELKANLHA
721 EPDYLEVLEQ QT

```

Figure 3C. Amino acid sequence 158P1D7 v.4 (SEQ ID NO: 16). The 158P1D7 v.4 protein has 395 amino acids.

```

1 MKLWIHLFYS SLLACISLHS QTPVLSSRGs CDSLNCNEEK DGTMLINCEA KGIKMVSEIS
61 VPPSRPFQLS LLNNGLTMLH TNDFSGLTNA ISIH LGFN NI ADIEIGAFNG LGLLKQLHIN
121 HNSLEILKED TFHGLENLEF LQADNNFITV IEPsAFsKLN RLKVLILNDN AIESLPPNIF
181 RFVPLTHLDL RGNQLQTLPY VGFLEHIGRI LDLQLEDNKW ACNCDLLQLK TWLENMPPQS
241 IIGDVVCNSP PFFKGSILSR LKKESICPTP PVYEEHEDPS GSLHLAATSS INDSRMSTKT

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301 TSILKLPTKA PGLIPYITKP STQLPGPYCP IPCNCKVLSP SGLLIHCQER NIESLSDLRP
361 PPQNPRKLIL AGNIIHSLMK SILWSKASGR

Figure 3D. Amino acid sequence 158P1D7 v.6 (SEQ ID NO: 17). The 158P1D7 v.6 protein has 529 amino acids.

1 MKLWIHLFYS SLLACISLHS QTPVLSSRGS CDSLNCNEEK DGTMLINCEA KGIKMVSEIS
61 VPPSRPFQLS LLNNGLTMLH TNDFSGLTNA ISIH LGFN NI ADIEIGAFNG LGLLKQLHIN
121 HNSLEILKED TFHGLLENLEF LQADNNFITV IEP SAFSKLN RLKVLILNDN AIESLPPNIF
181 RFVPLTHLDL RGNQLQTLPY VGFLEHIGRI LDLQLEDNKW ACNCDLLQLK TWLENMPPQS
241 IIGDVVCNSP PFFKGSILSR LKKESICPTP PVYEEHEDPS GSLHLAATSS INDSRMSTKT
301 TSILKLPTKA PGLIPYITKP STQLPGPYCP IPCNCKVLSP SGLLIHCQER NIESLSDLRP
361 PPQNPRKLIL AGNIIHSLMN PSFGPKHLEE EEERNEKEGS DAKHLQRSLL EQENHSPLTG
421 SNMKYKTTNQ STEFLSFQDA SSLYRNILEK ERELQQLGIT EYLRKNIAQL QPDMEAHYPG
481 AHEELKLMET LMYSRPRKVL VEQTKNEYFE LKANLHAEPD YLEVLEQQT

Figure 4: 158P1D7 v.1 amino acid (SEQ ID NO: 18) BLAST homology to hypothetical protein FLJ22774 (SEQ ID NO: 19).

Identities = 798/798 (100%)

Query: 44 MLINCEAKGIKMVSEISVPPSRPFQSLNNGLTMLHTNDFSGLTNAISIHGFGNNIADI 103
MLINCEAKGIKMVSEISVPPSRPFQSLNNGLTMLHTNDFSGLTNAISIHGFGNNIADI
Sbjct: 1 MLINCEAKGIKMVSEISVPPSRPFQSLNNGLTMLHTNDFSGLTNAISIHGFGNNIADI 60

Query: 104 EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLK 163
EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLK
Sbjct: 61 EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLK 120

Query: 164 VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPYVGFLEHIGRILDQLEDNKWACN 223
VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPYVGFLEHIGRILDQLEDNKWACN
Sbjct: 121 VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPYVGFLEHIGRILDQLEDNKWACN 180

Query: 224 CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRLKKEICPTPPVYEEHEDPSGSL 283
CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRLKKEICPTPPVYEEHEDPSGSL
Sbjct: 181 CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRLKKEICPTPPVYEEHEDPSGSL 240

Query: 284 HLAATSSINDSRMSTKTTSSILKLPKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL 343
HLAATSSINDSRMSTKTTSSILKLPKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL
Sbjct: 241 HLAATSSINDSRMSTKTTSSILKLPKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL 300

Query: 344 LIHCQERNIESLSDLRPPQNPRKLILAGNIIHSLMKSDLVEYFTLEMLHLGNNRIEVLE 403
LIHCQERNIESLSDLRPPQNPRKLILAGNIIHSLMKSDLVEYFTLEMLHLGNNRIEVLE
Sbjct: 301 LIHCQERNIESLSDLRPPQNPRKLILAGNIIHSLMKSDLVEYFTLEMLHLGNNRIEVLE 360

Query: 404 EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHNLEYLYLEYNAIKEILPGTFNPMPLKV 463
EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHNLEYLYLEYNAIKEILPGTFNPMPLKV
Sbjct: 361 EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHNLEYLYLEYNAIKEILPGTFNPMPLKV 420

Query: 464 LYLNNNLLQVLPPHIFSGVPLTKVNLKTNQFTHLPVSNILDDLDTQIDLEDNPWDCSC 523
LYLNNNLLQVLPPHIFSGVPLTKVNLKTNQFTHLPVSNILDDLDTQIDLEDNPWDCSC
Sbjct: 421 LYLNNNLLQVLPPHIFSGVPLTKVNLKTNQFTHLPVSNILDDLDTQIDLEDNPWDCSC 480

Query: 524 DLVGLQQWIQKLSKNTVTDDILCTSPGHLDKKELKALNSEILCPGLVNNPSMPTQTSYLM 583
DLVGLQQWIQKLSKNTVTDDILCTSPGHLDKKELKALNSEILCPGLVNNPSMPTQTSYLM
Sbjct: 481 DLVGLQQWIQKLSKNTVTDDILCTSPGHLDKKELKALNSEILCPGLVNNPSMPTQTSYLM 540

Query: 584 VTTPTTTNTADTILRSLTDAVPLSVLILGLLIMFITIVFCAAGIVVLVHRRRRYKKKQ 643
VTTPTTTNTADTILRSLTDAVPLSVLILGLLIMFITIVFCAAGIVVLVHRRRRYKKKQ
Sbjct: 541 VTTPTTTNTADTILRSLTDAVPLSVLILGLLIMFITIVFCAAGIVVLVHRRRRYKKKQ 600

Query: 644 VDEQMRDNSPVHLQYSMYGHKTTHTTTERPSASLYEQHMVSPMVHVYRSPSFGPKHLEEE 703
VDEQMRDNSPVHLQYSMYGHKTTHTTTERPSASLYEQHMVSPMVHVYRSPSFGPKHLEEE
Sbjct: 601 VDEQMRDNSPVHLQYSMYGHKTTHTTTERPSASLYEQHMVSPMVHVYRSPSFGPKHLEEE 660

Query: 704 EERNEKEGSDAKHLQRLLEQENHSPLTGSNMKYKTTNQSTEFLSFQDASSLYRNILEKE 763
EERNEKEGSDAKHLQRLLEQENHSPLTGSNMKYKTTNQSTEFLSFQDASSLYRNILEKE
Sbjct: 661 EERNEKEGSDAKHLQRLLEQENHSPLTGSNMKYKTTNQSTEFLSFQDASSLYRNILEKE 720

Query: 764 RELQQLGITEYLRKNIAQLQPDMEAHYPGAHEELKLMETLMYSRPRKVLVEQTKNEYFEL 823
RELQQLGITEYLRKNIAQLQPDMEAHYPGAHEELKLMETLMYSRPRKVLVEQTKNEYFEL
Sbjct: 721 RELQQLGITEYLRKNIAQLQPDMEAHYPGAHEELKLMETLMYSRPRKVLVEQTKNEYFEL 780

Query: 824 KANLHAEPDYLEVLEQQT 841
KANLHAEPDYLEVLEQQT
Sbjct: 781 KANLHAEPDYLEVLEQQT 798

Figure 5:

Figure 5A: Alignment of 158P1D7 v.1 (SEQ ID NO: 20) with human FLJ22774, CLONE KAIA1575.[Homo sapiens] (SEQ ID NO: 21)

Identities = 405/415 (97%), Positives = 405/415 (97%)

```

158P1D7: 44 MLINCEAKGIKMVSEISVPPSRPFQLSLLNGLTMLHTNDFSGLTNAISIHGFMNIADI 103
              MLINCEAKGIKMVSEISVPPSRPFQLSLLNGLTMLHTNDFSGLTNAISIHGFMNIADI
Sbjct: 1      MLINCEAKGIKMVSEISVPPSRPFQLSLLNGLTMLHTNDFSGLTNAISIHGFMNIADI 60

158P1D7:104 EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENEFLQADNNFITVIEPSAFSKLNRLK 163
              EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENEFLQADNNFITVIEPSAFSKLNRLK
Sbjct: 61     EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENEFLQADNNFITVIEPSAFSKLNRLK 120

158P1D7:164 VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPHYVGFLEHIGRILDQLQEDNKWACN 223
              VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPHYVGFLEHIGRILDQLQEDNKWACN
Sbjct: 121    VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPHYVGFLEHIGRILDQLQEDNKWACN 180

158P1D7:224 CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRLKKESICPTPPVYEEHEDPSGSL 283
              CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRLKKESICPTPPVYEEHEDPSGSL
Sbjct: 181    CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRLKKESICPTPPVYEEHEDPSGSL 240

158P1D7:284 HLAATSSINDSRMSTKTTSSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL 343
              HLAATSSINDSRMSTKTTSSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL
Sbjct: 241    HLAATSSINDSRMSTKTTSSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL 300

158P1D7:344 LIHCQERNIESLSDLRPPQNPRLILAGNIIHSLMKSDLVEYFTLEMLHLGNRNRIEVL 403
              LIHCQERNIESLSDLRPPQNPRLILAGNIIHSLMKSDLVEYFTLEMLHLGNRNRIEVL
Sbjct: 301    LIHCQERNIESLSDLRPPQNPRLILAGNIIHSLMKSDLVEYFTLEMLHLGNRNRIEVL 360

158P1D7:404 EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHXXXXXXXXXXAIKEILPGTFNPM 458
              EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLH AIKEILPGTFNPM
Sbjct: 361    EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHNLLEYLYLEYNAIKEILPGTFNPM 415

```

Figure 5b: Alignment of 158P1D7 v.1 protein (SEQ ID NO: 22) with a human protein similar to IGFALS (SEQ ID NO: 23)

Identities = 316/864 (36%), Positives = 459/864 (52%)

```

158P1D7:1  MKLWIHLFYSSLLACISLHSQTPVLSSRGSCDSLNCCEKDGTM LINCEAKGIKMVSEIS 60
              M LW+ L S+L++ + S V ++C+C + + +NCE + +++
Sbjct: 17  MFLWLFLILSALISSTNADSDISV-----EICNVCSVCVSVENVLYVNCVKSVYRPNQLK 71

158P1D7:61  VPPSRPFQLSLLNGLTMLHTNDFSGLTNAISIHGFMNIADIEIGAFNGLGLLKQLHIN 120
              P S + L+ NN L +L+ N F ++A+S+HLG N + +IE GAF GL LKQLH+N
Sbjct: 72  PPWSNFYHLNFQNNFLNLYPNTFLNFHAVSLHLGNNKLQNIEGGAFLGLSALKQLHLN 131

158P1D7:121 HNSLEILKEDTFHGLENEFLQADNNFITVIEPSAFSKLNRLKVLILNDNAIESLPPNIF 180
              +N L+IL+ DTF G+ENLE+LQAD N I IE AF+KL++LKVLILNDN I LP NIF
Sbjct: 132  NNELKILRADTFGLGLENLEYLQADYNLIKYIERGAFNKLHLKVLILNDNLISFLPDNIF 191

158P1D7:181 RFVPLTHLDLRGNQLQTLPHYVGFLEHIGRILDQLQEDNKWACNCDLLQLKTWLENMPPQS 240
              RF LTHLD+RGN++Q LPY+G LEHIGR+++LQLEDN W C+CDLL LK WLENMP
Sbjct: 192  RFASLTHLDIRGNRIQKLPYIGVLEHIGRVVELQLEDNPWNCSDLLPLKAWLENMPYNI 251

158P1D7:241 IIGDVVCNSPPFFKGSILSRLKKESICP-----TPPVYEEHEDPSGSLHLAATS 289
              IG+ +C +P G +L K+ +CP PP E+ + + H TS
Sbjct: 252  YIGEAICTPSDLYGRLLKETNKQELCPMGTSDFDVRILPPSQLENGYTTPNGHTTQTS 311

158P1D7:290 SINDSRMSTKTTSSILKLPTKAPGLI-----PYITKPSTQLPG-PYCPIPCNCKV- 337
              KTT+ P+K G++ I T++P CP PC CK
Sbjct: 312  LHRLVTKPKPTTN----PSKISGIVAGKALSNNRNLQIVSYQTRVPLTPCPAPCFCKTH 367

158P1D7:338 LSPSGLLIHCQERNIESLSDLRPPQNPRLILAGNIIHSLMKSDLVEYFTLEMLHLGN 397
              S GL ++CQE+NI+S+S+L P P N +KL + GN I + SD ++ L++LHLG+N
Sbjct: 368  PSDLGLSVNCQEKNIQSMSELIPKPLNAKHLHVNGNSIKDQVDVDFDTDFEGLDLLHLGSN 427

158P1D7:398 RIEVLEEGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHXXXXXXXXXXAIKEILPGTFNP 457
              +I V++ F NLT L++LYLNGN + +L +F GLH IKEI GTF+
Sbjct: 428  QITVIKGDVFNHNLNLRRLYLNGNQIERLYPEIFSGLHNLQYLYLEYNLIKEISAGTFDS 487

```

158P1D7:458 MXXXXXXXXXXXXXXXXXHFSGVPLTKVNLKTNQFTHLPVSNIXXXXXXXXXXXXXXN 517
M +IFSG PL ++NL+ N+F +LPVS + N
Sbjct: 488 MPNLQLLYLNNNLLKSLPVYIFSGAPLARLNLNRNNKFMVLPVSGVLDQLQSLTQIDLEGN 547

158P1D7:518 PWDCSCDLVGLQQWIQKLSKNTVTDDILCTSPGHLDDKKELKALNSEILCPGLVNNPSMPT 577
PWDC+CDLV L+ W++KLS V ++ C +P ELK+L +EILCP L+N PS P
Sbjct: 548 PWDCTCDLVALKLWVEKLSDGIVVKELKCETPVQFANIELKSLKNEILCPKLLNKPSAP- 606

158P1D7:578 QTSYLMVXXXXXXXXXXXXXILRSLTDAVPLSVLILGLLIMFITIVFCAAGIVVLVLRHRR 637
+ I VPLS+LIL +L++ I VF A ++V VL R +
Sbjct: 607 ---FTSPAPAITFTTPLGPIRSPPGGPVPLSILILSILVVLILTTFVAFCLLVFLRRNK 663

158P1D7:638 RYKKKQVDEQMRDNSPVHLQYSMYGHKTTHHTTERPSASLYEQHVMVSPMVHVYRSPSFGP 697
+ K D + LQ + HK T + E + + +S + G
Sbjct: 664 KPVTVKHEGLGNPDGSMQLQLRKHDHK-----TNKKDGLSTEAFIPQTIEQMSKSHTCGL 718

158P1D7:698 KHLXXXXXXXXXXGSDAKHLQRSLLSEQENHSPLTGSNMKYKTTNQSTEFSLFQDASSLYR 757
K G K + R++ ++E + + T ++ E +D++ +
Sbjct: 719 KESETGFMFSDPPGQ--KVMRNVADKEKDLLHVDTRKRLSTIDELDELFP SRDSNVFIQ 776

158P1D7:758 NILEKERELQQLGITEYLRKNIAQLQPDMEAHYPGAHEELKLMETLMYSRPRKVLVEQTK 817
N LE ++E +G++ + E YP + K ++L+ K++VEQ K
Sbjct: 777 NFLESKKEYNSIGVSGF-----EIRYPEKQPDKSKKSLIGNHNSKIVVEQRK 824

158P1D7:818 NEYFELKANLHAEPDYLEVLEQQT 841
+EYFELKA L + PDYL+VLE+QT
Sbjct: 825 SEYFELKAKLQSSPDYLQVLEEQT 848

Figure 6. Expression of 158P1D7 by RT-PCR

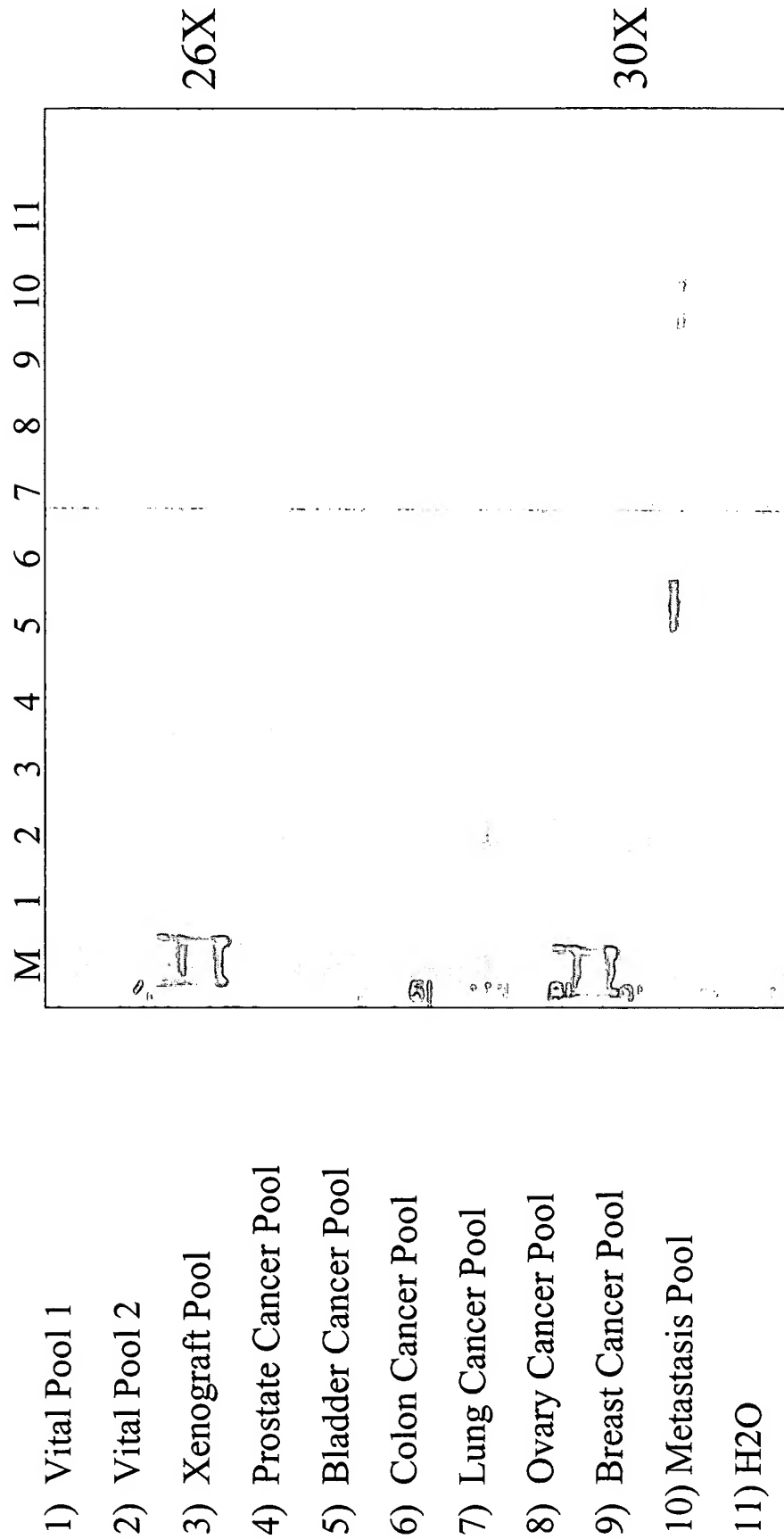


Figure 7. Expression of 158P1D7 in Normal Tissues

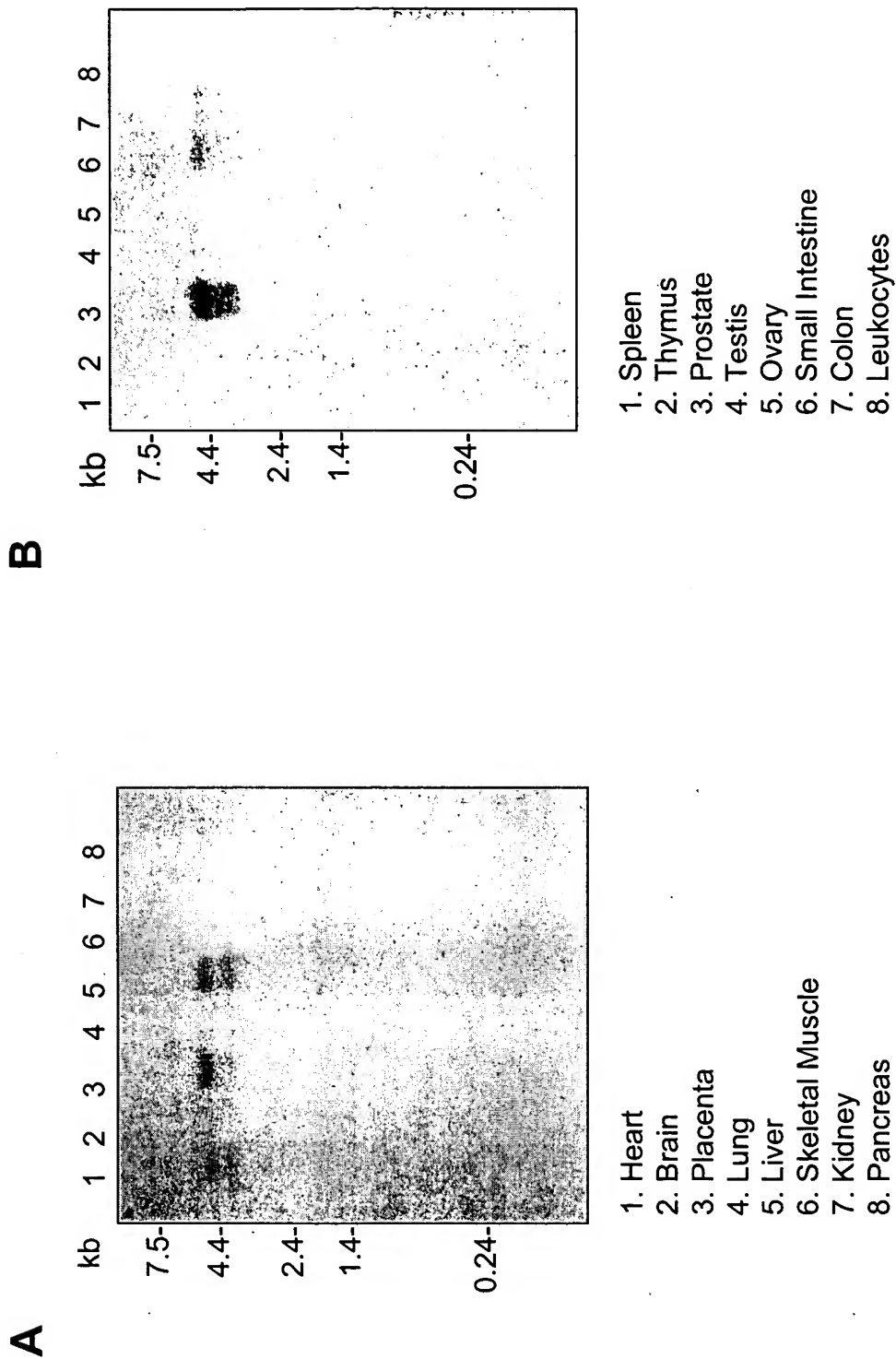
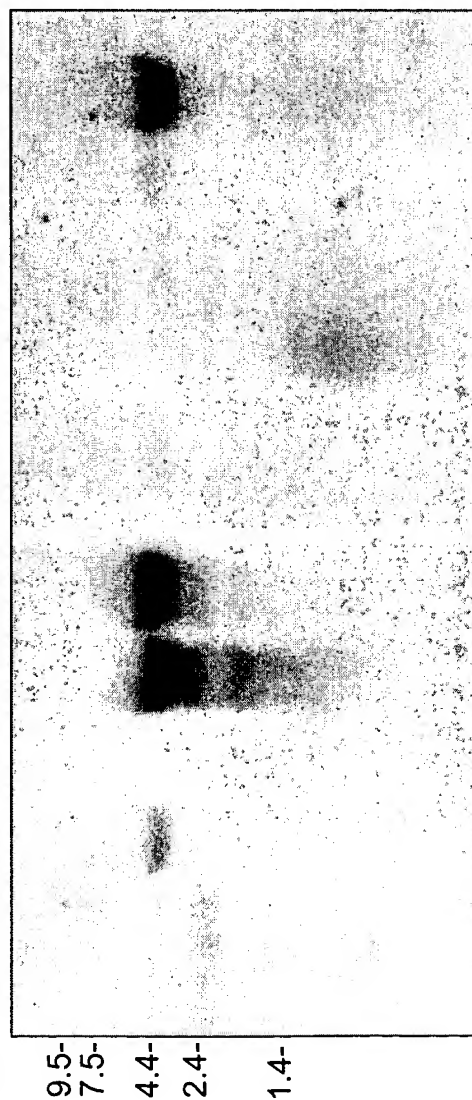


Figure 8A. Expression of 158P1D7 in Bladder Cancer Patient Specimens

	P1	P2	P3	P4	P5	P6
kb	CL	CL	CL	N	NAT	T
	NAT	T	NAT	T	T	T



P1 - Transitional, grade 4

P2 - Squamous inv.

P3 - Transitional, grade 3

P4 - Papillary non -inv, grade 1/3

P5 - Papillary, grade 3/3

P6 - Transitional, grade 3/2

CL = Cell lines (listed in order): UM-UC-3, J82, SCaBER

P = Patient

N = Normal Bladder

***NAT* = Normal adjacent tissue**

$$T = \textit{Tumor}$$

Figure 8B. Expression of 158P1D7 in Bladder Cancer Patient Specimens

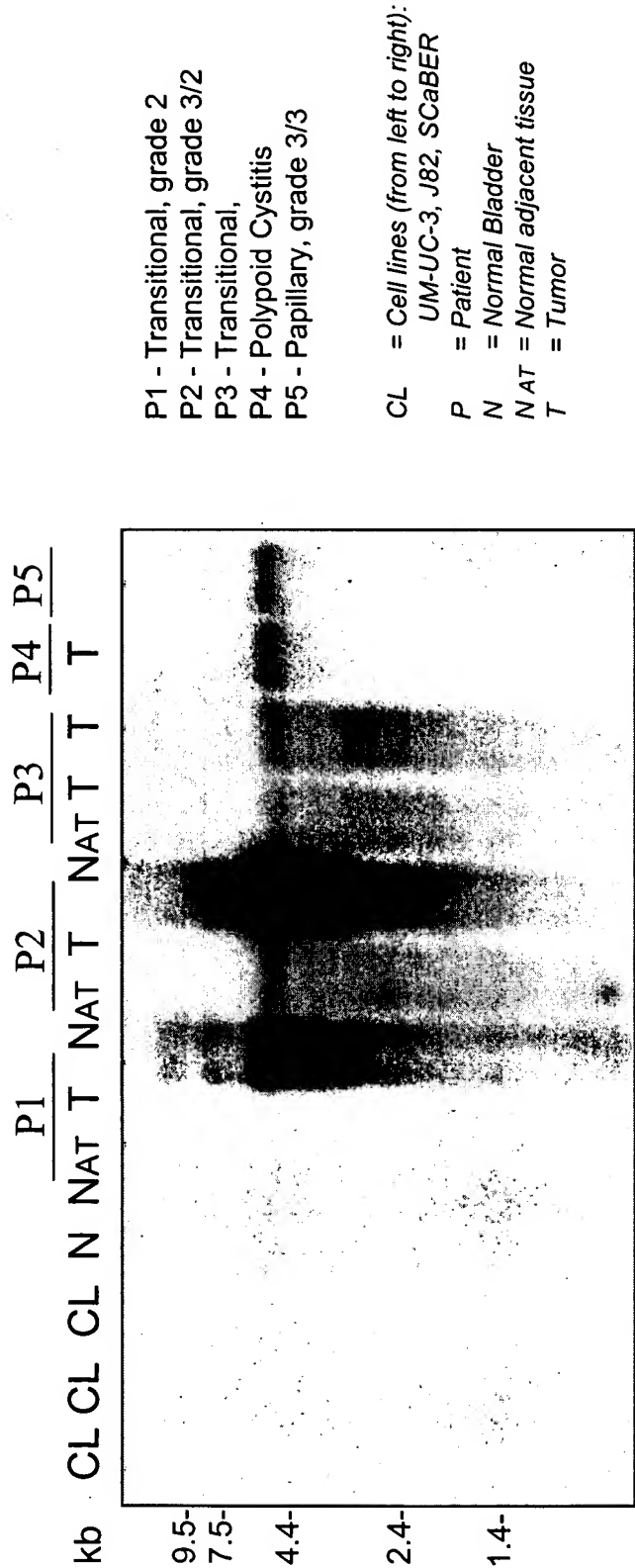


Figure 9.

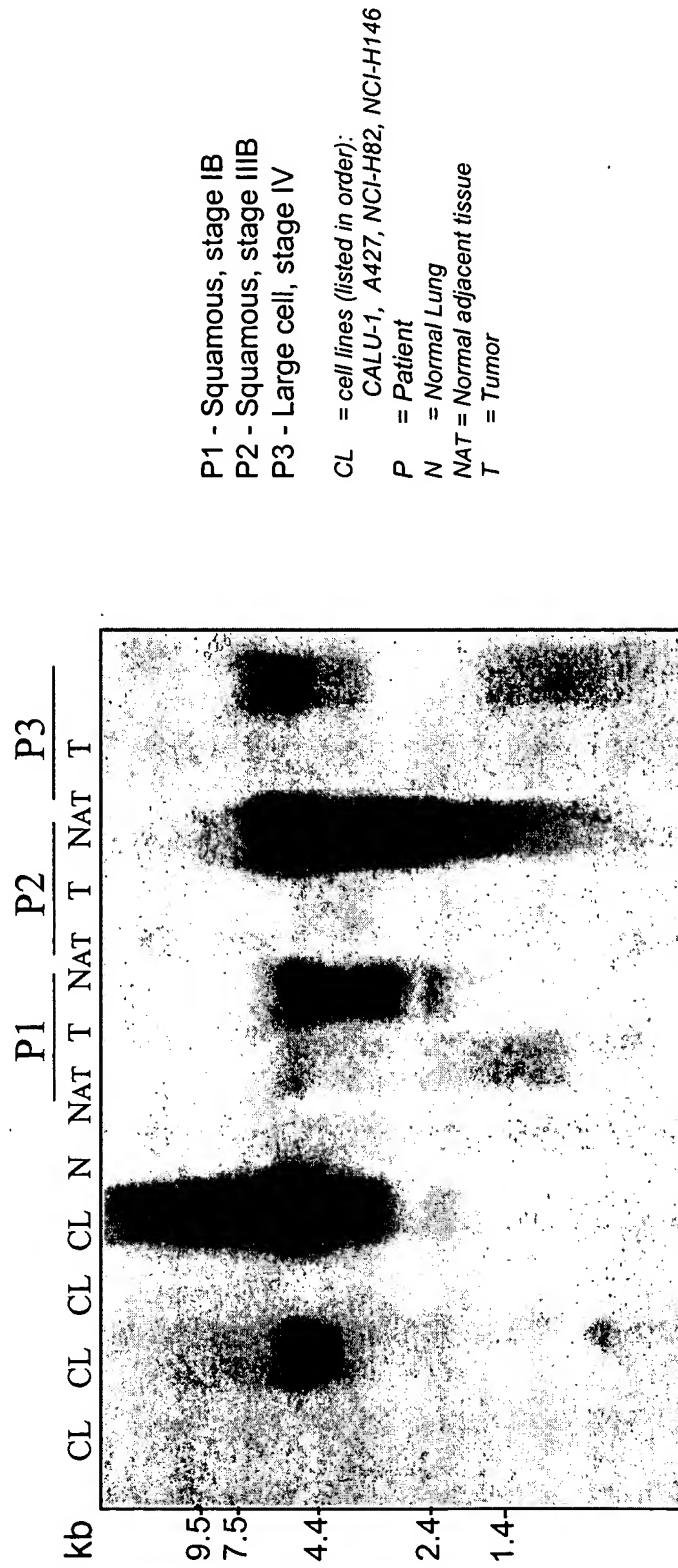


Figure 10. Expression of 158P1D7 in Breast Cancer Patient Specimens

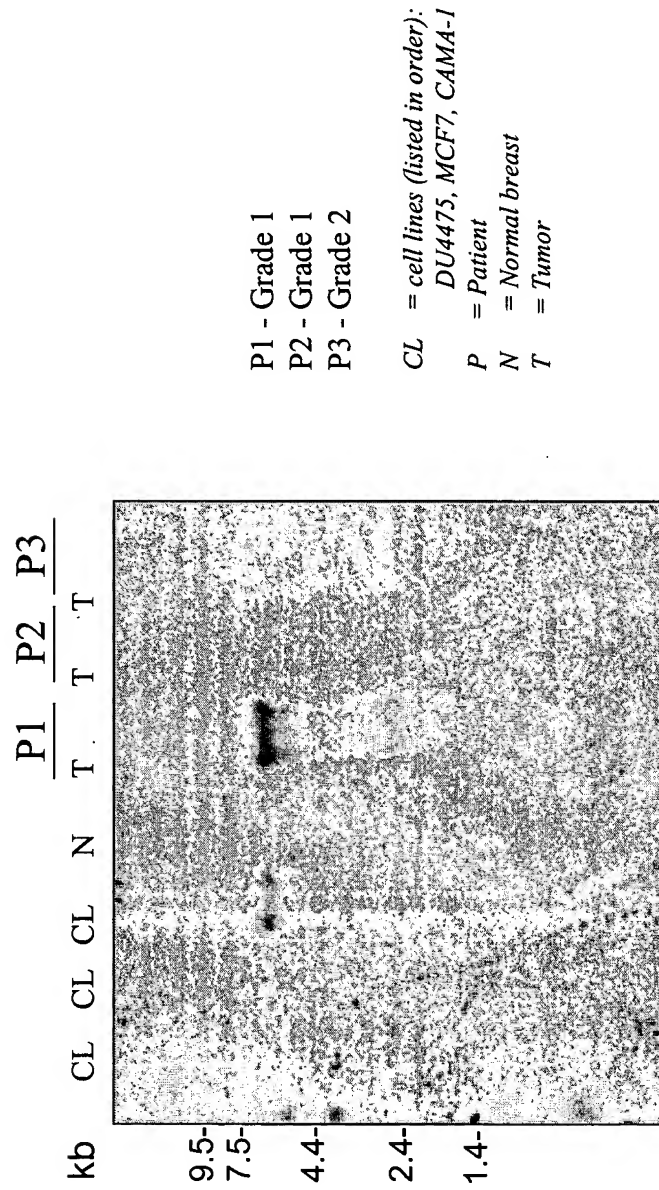


Figure 11a - 158P1D7 variant 1

Hydrophilicity profile

(Hopp T.P., Woods K.R., 1981.
Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

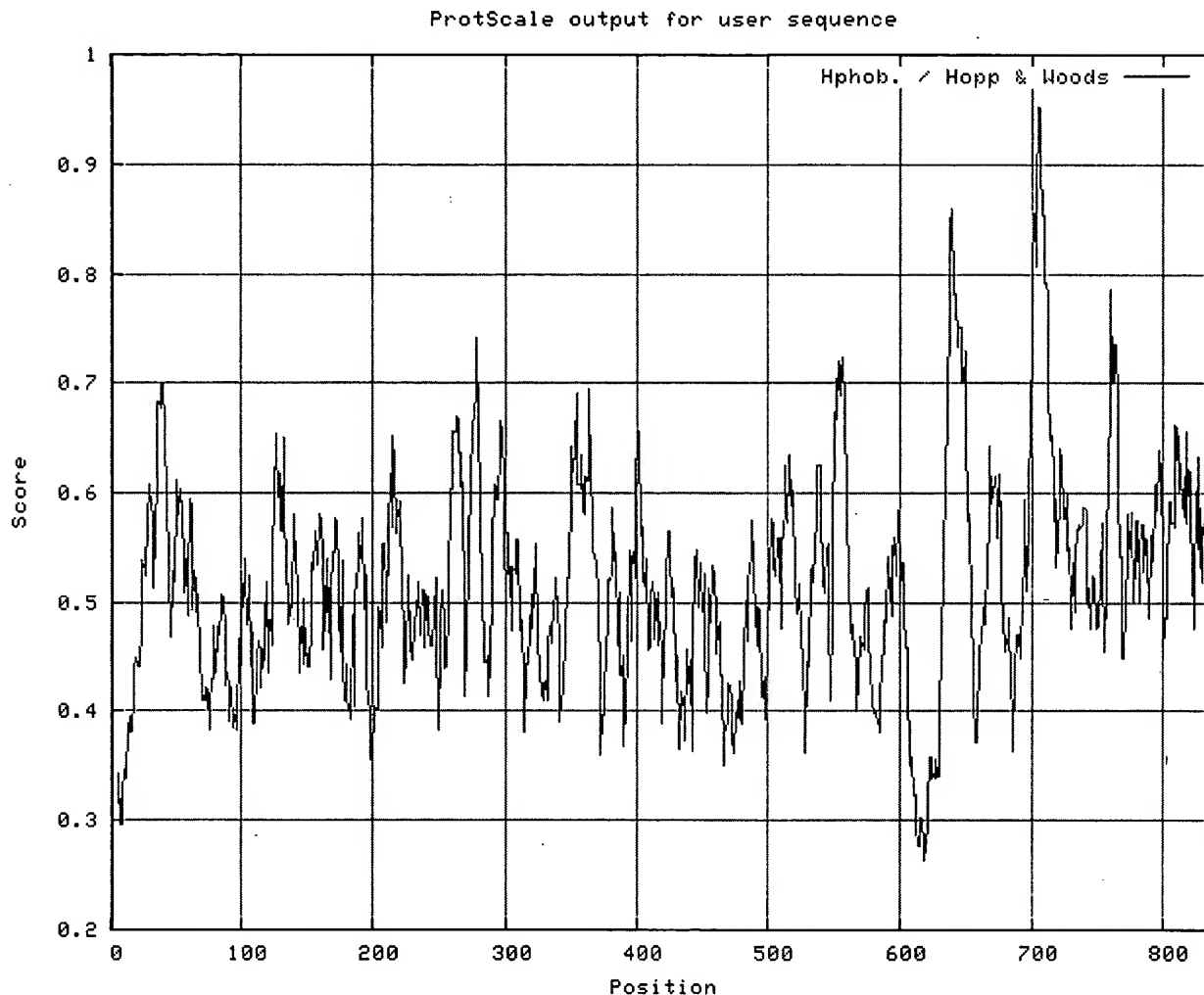


Figure 11b - 158P1D7 variant 3

Hydrophilicity profile

(Hopp T.P., Woods K.R., 1981.
Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

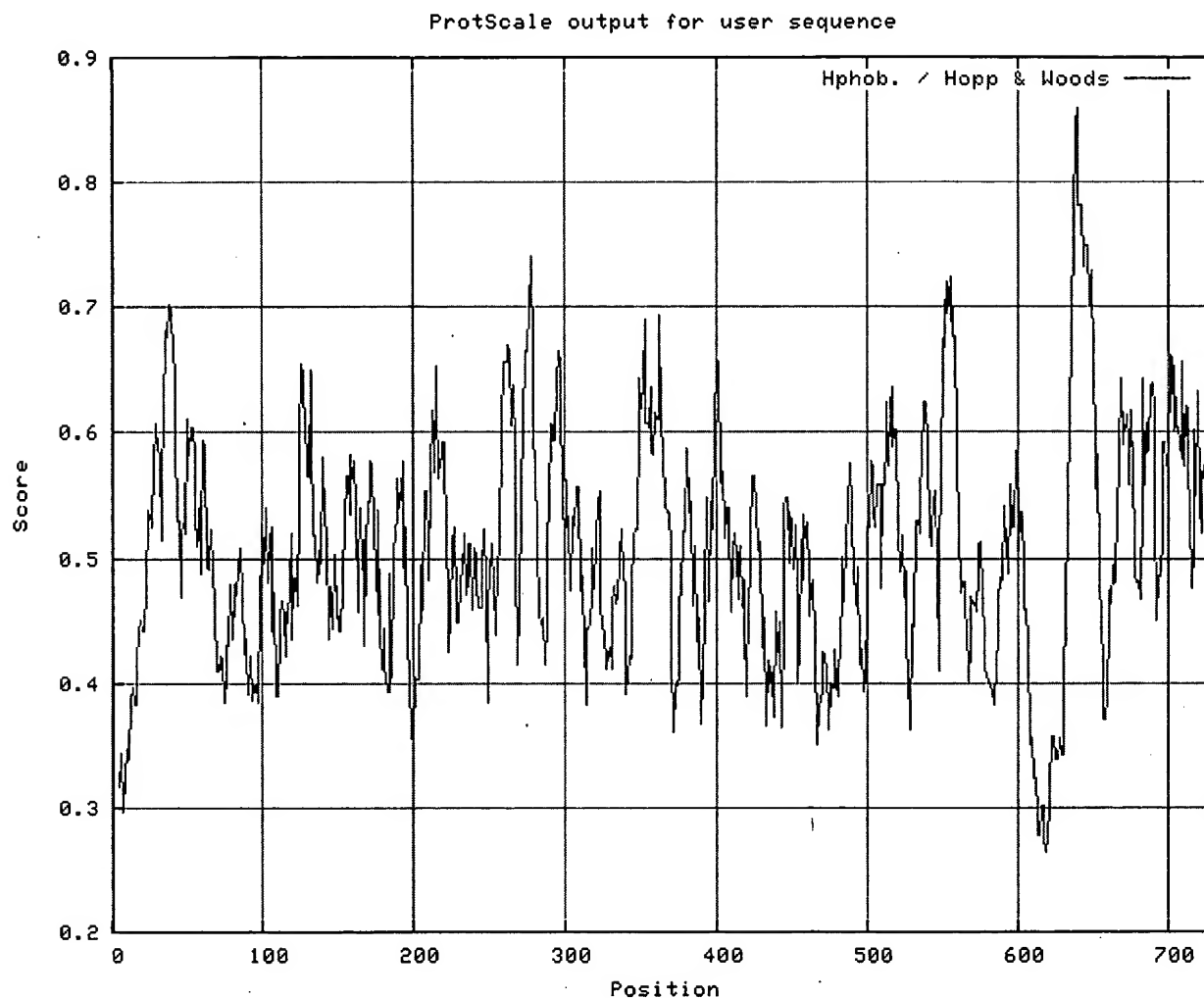


Figure 11c - 158P1D7 variant 4
Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981.
Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

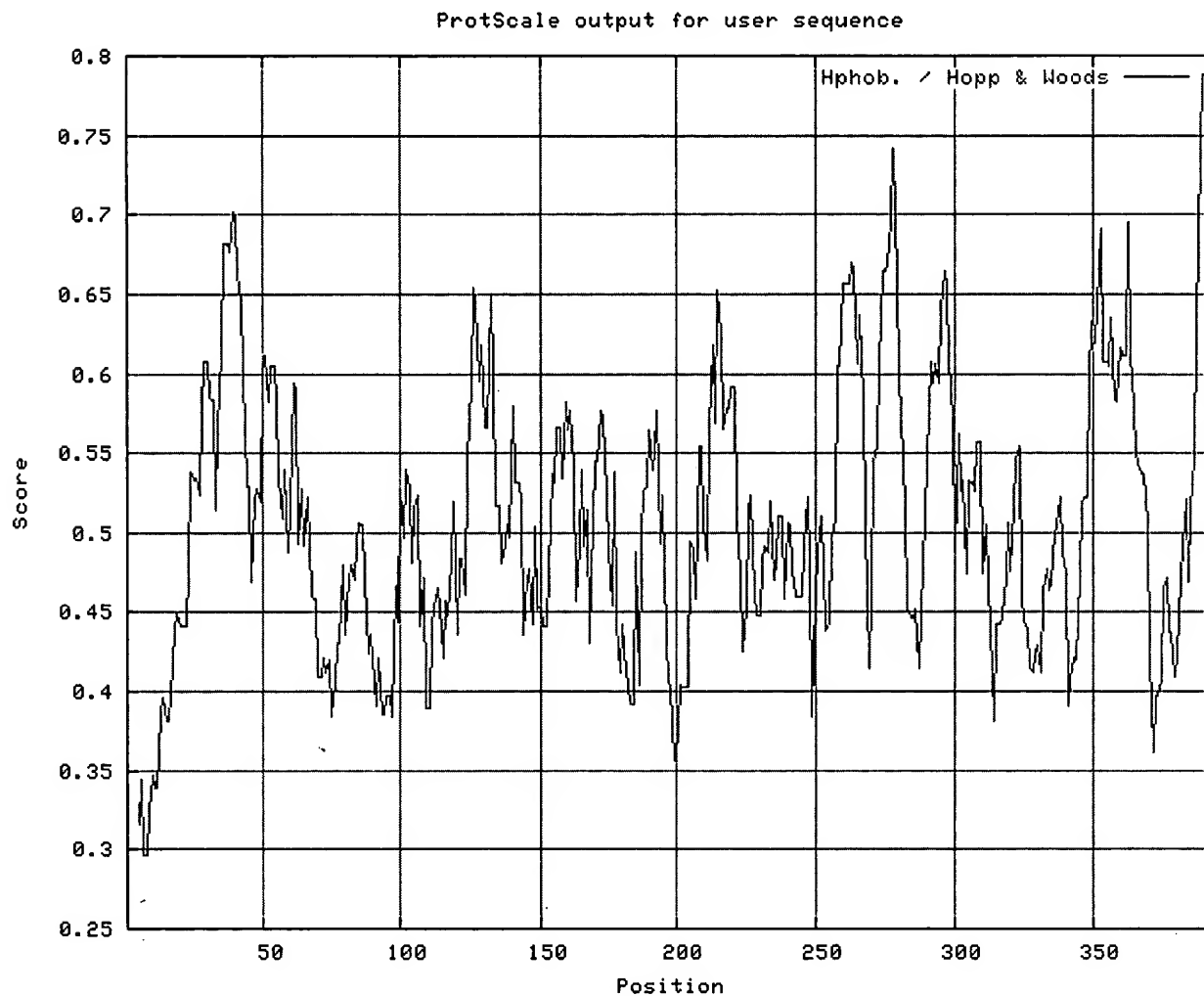


Figure 11d - 158P1D7 variant 6

Hydrophilicity profile

(Hopp T.P., Woods K.R., 1981.

Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

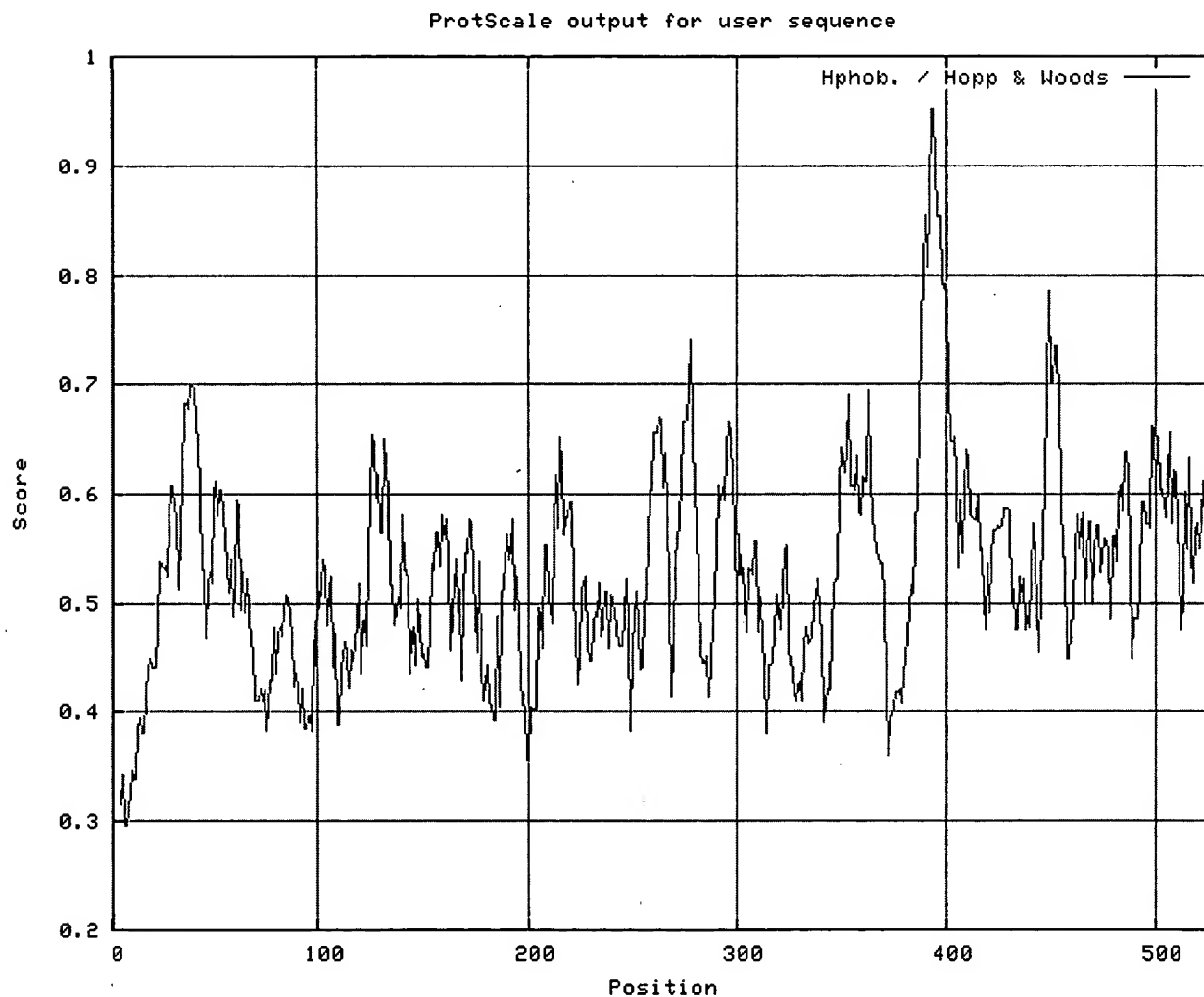


Figure 12a - 158P1D7 variant 1

Hydropathicity Profile

(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

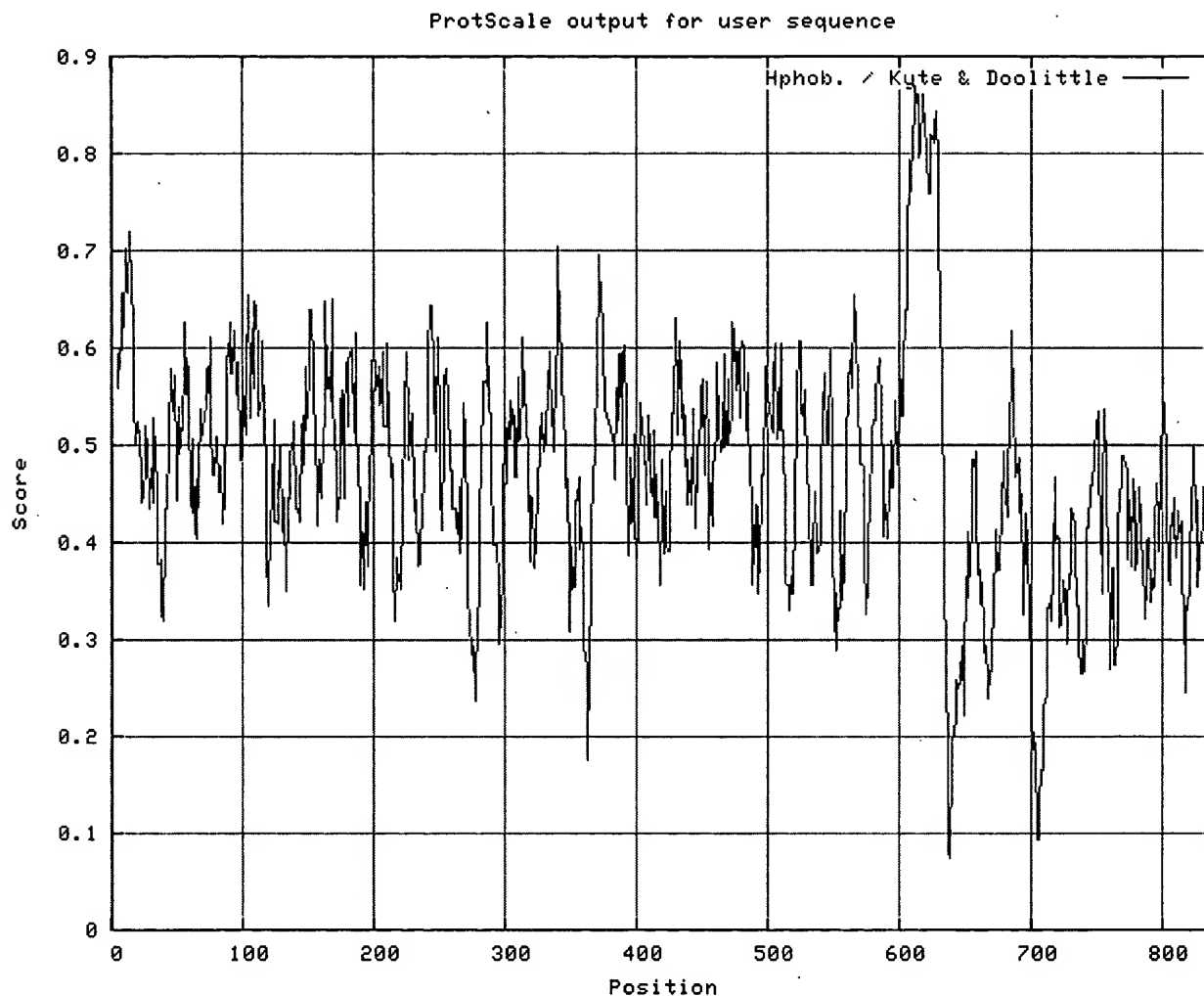


Figure 12b - 158P1D7 variant 3

Hydropathicity Profile

(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

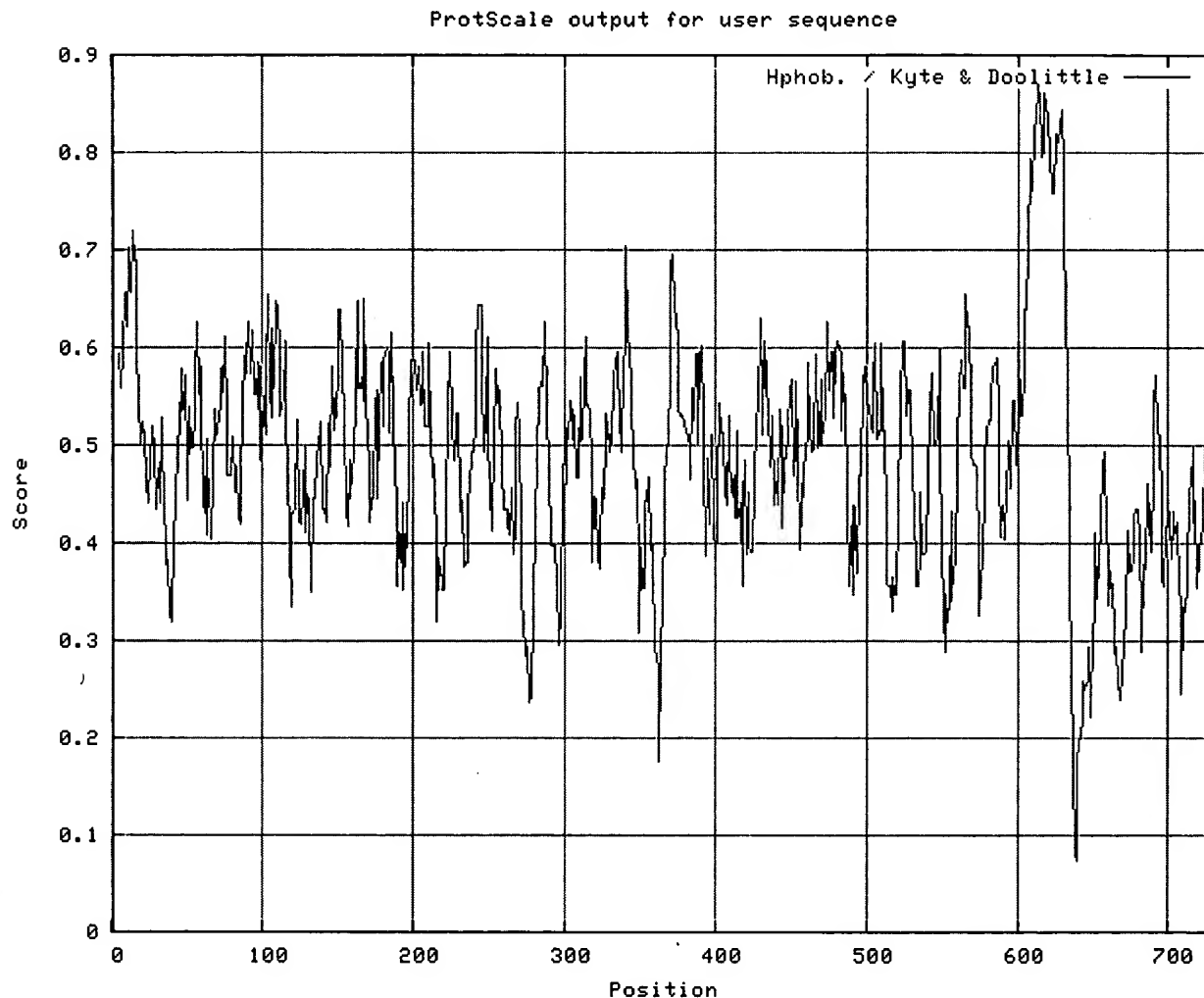


Figure 12c - 158P1D7 variant 4

Hydropathicity Profile

(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

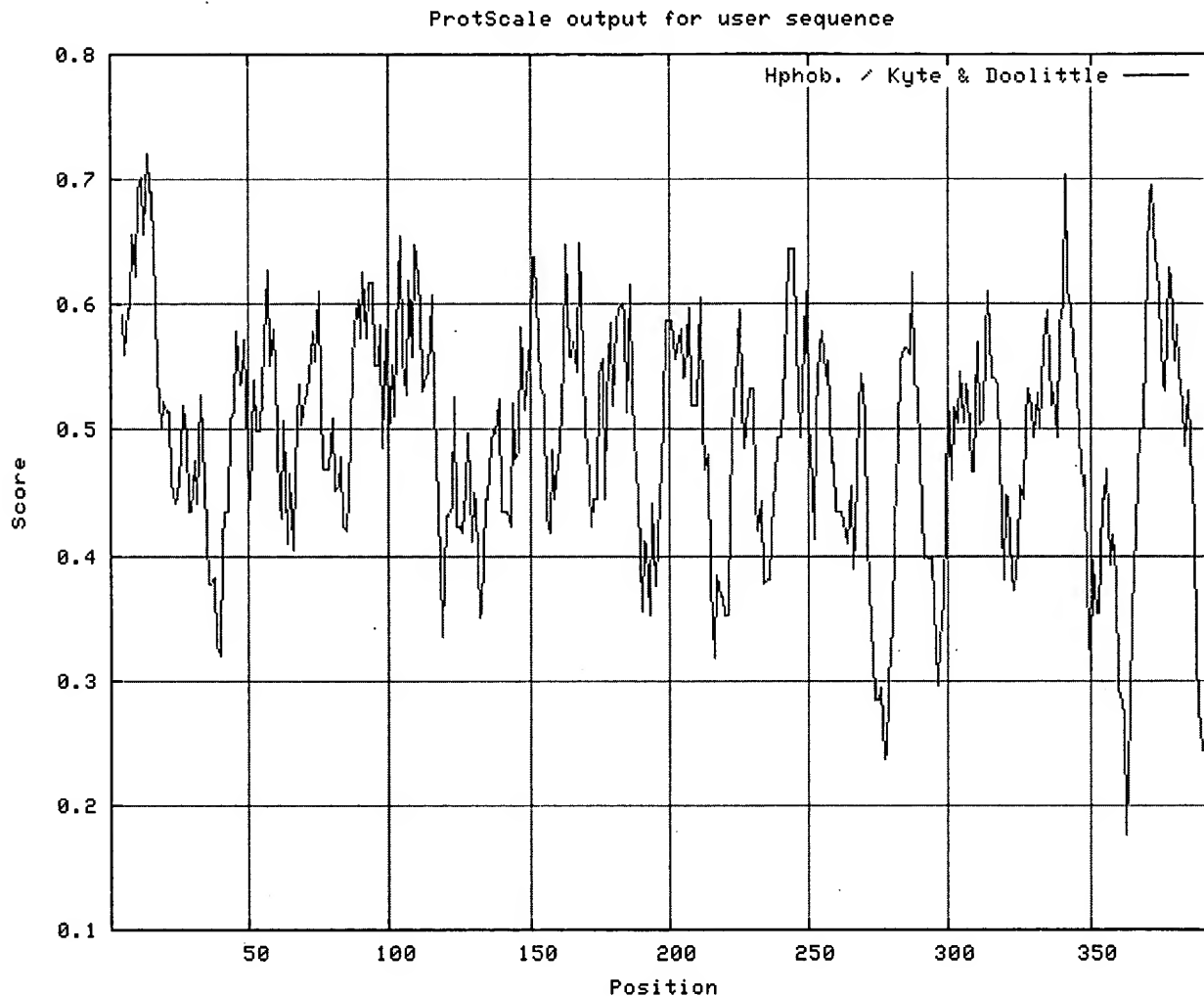


Figure 12d - 158P1D7 variant 6

Hydropathicity Profile

(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

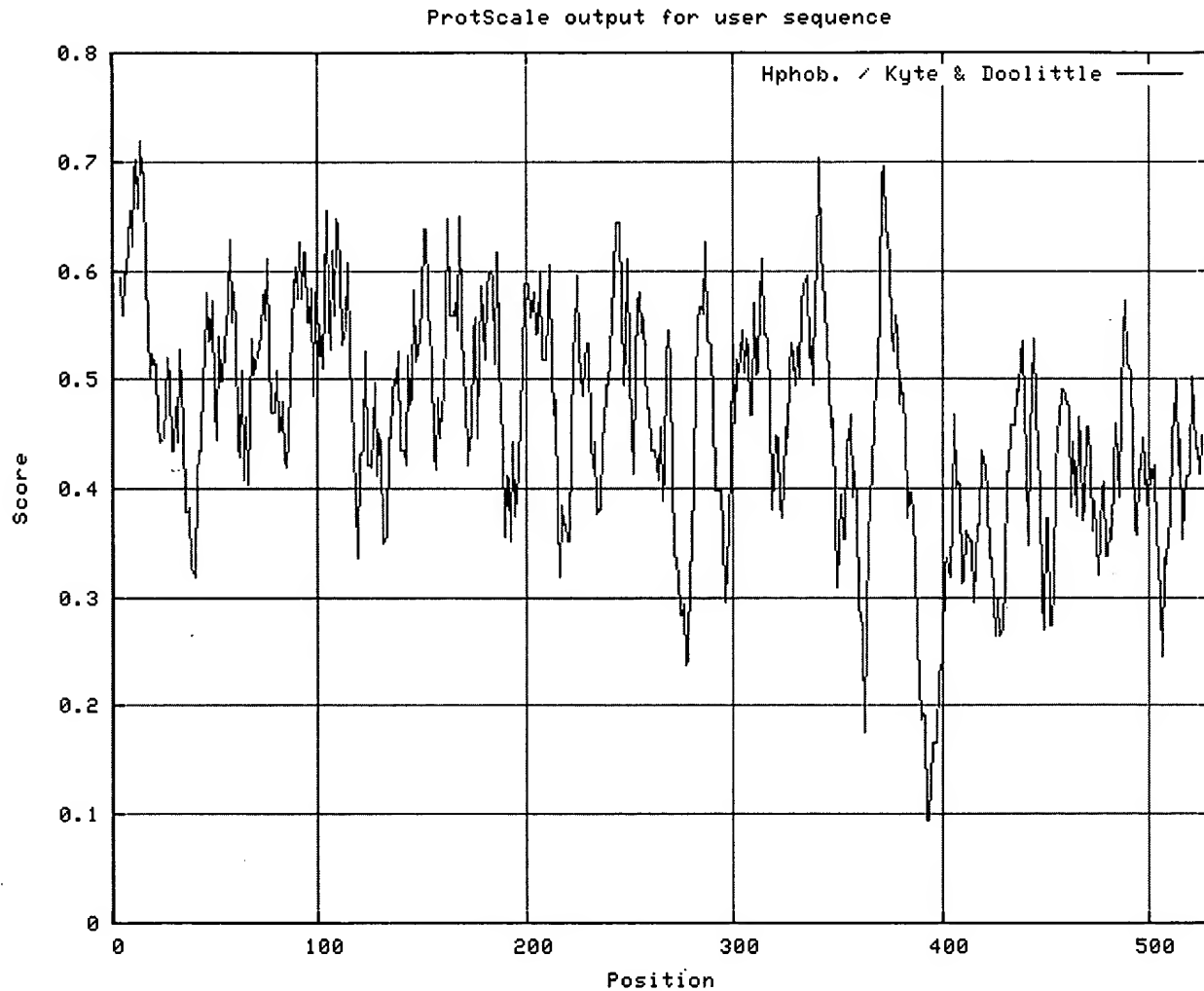


Figure 13a - 158P1D7 variant 1 % Accessible Residues Profile (Janin J., 1979. Nature 277:491-492)

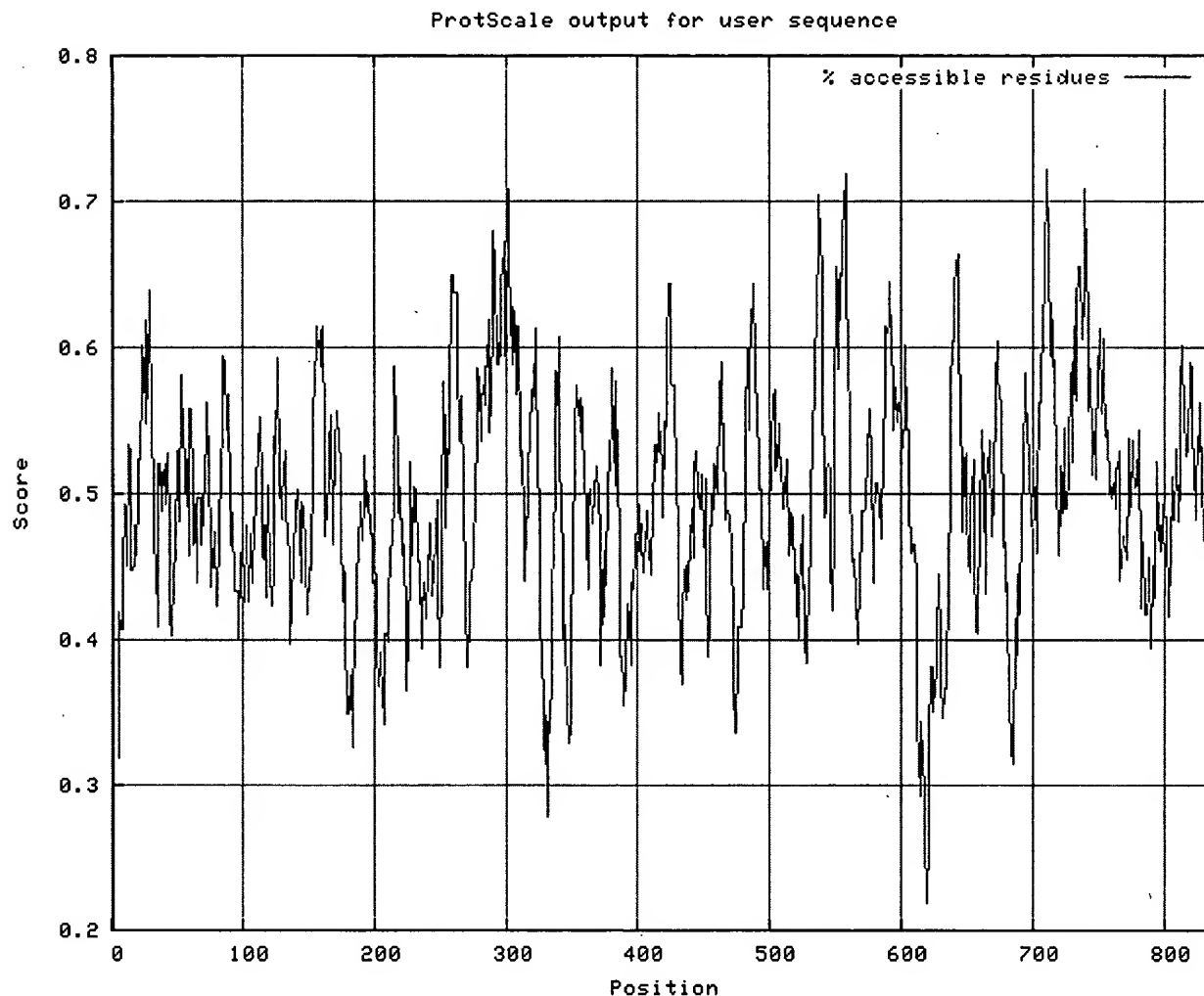


Figure 13b - 158P1D7 variant 3 % Accessible Residues Profile (Janin J., 1979. Nature 277:491-492)

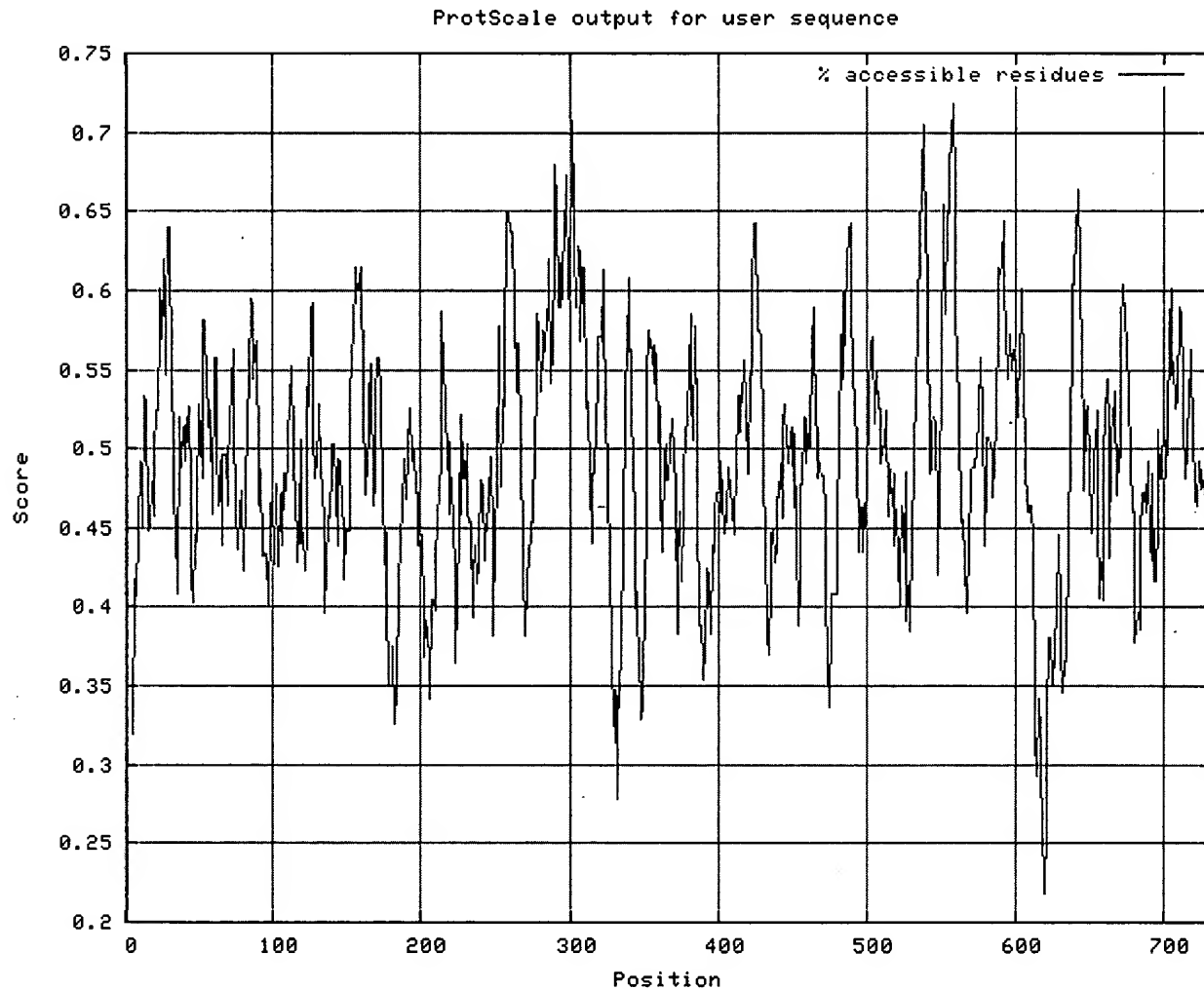


Figure 13c - 158P1D7 variant 4 % Accessible Residues Profile (Janin J., 1979. Nature 277:491-492)

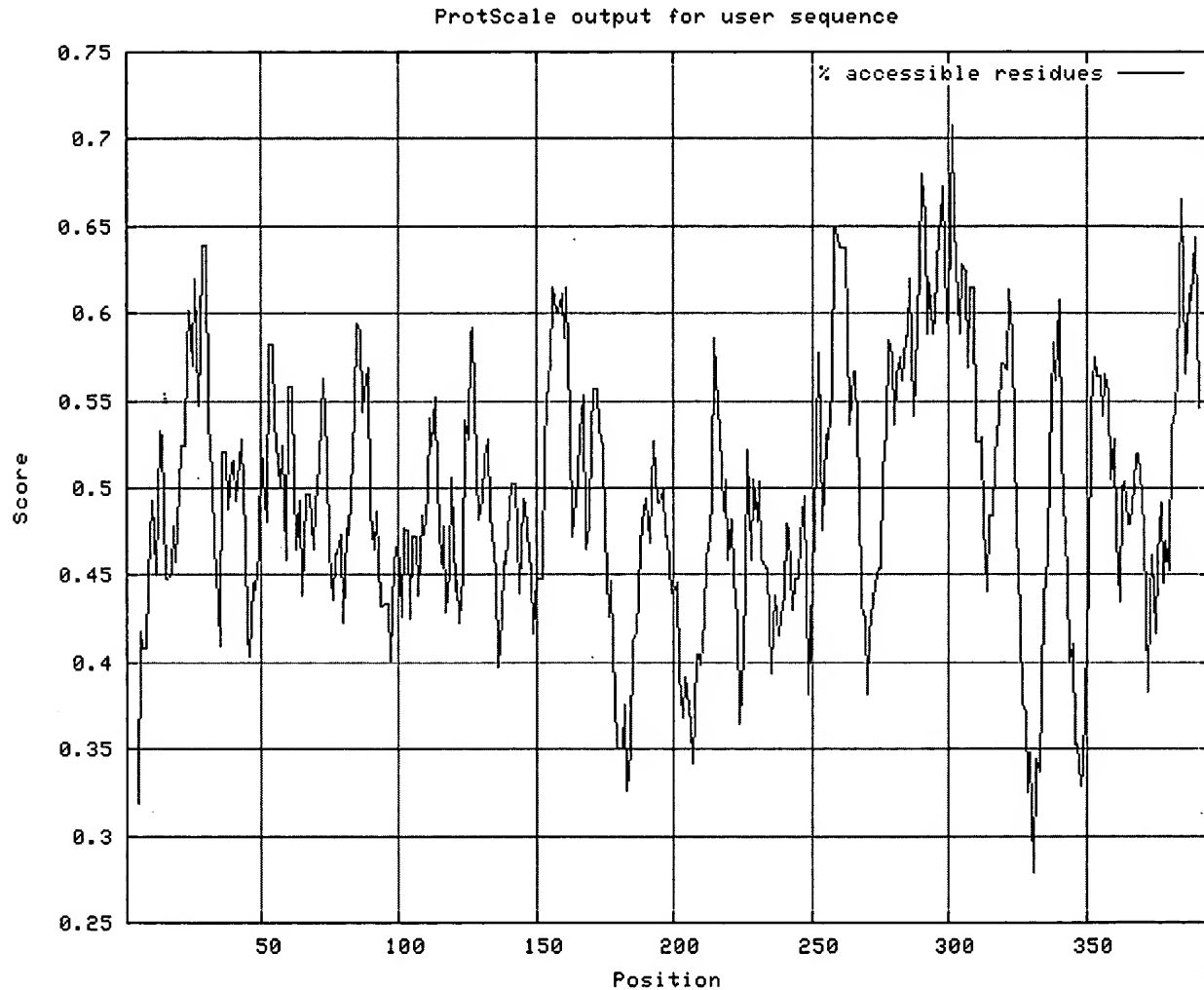


Figure 13d - 158P1D7 variant 6 % Accessible Residues Profile (Janin J., 1979. Nature 277:491-492)

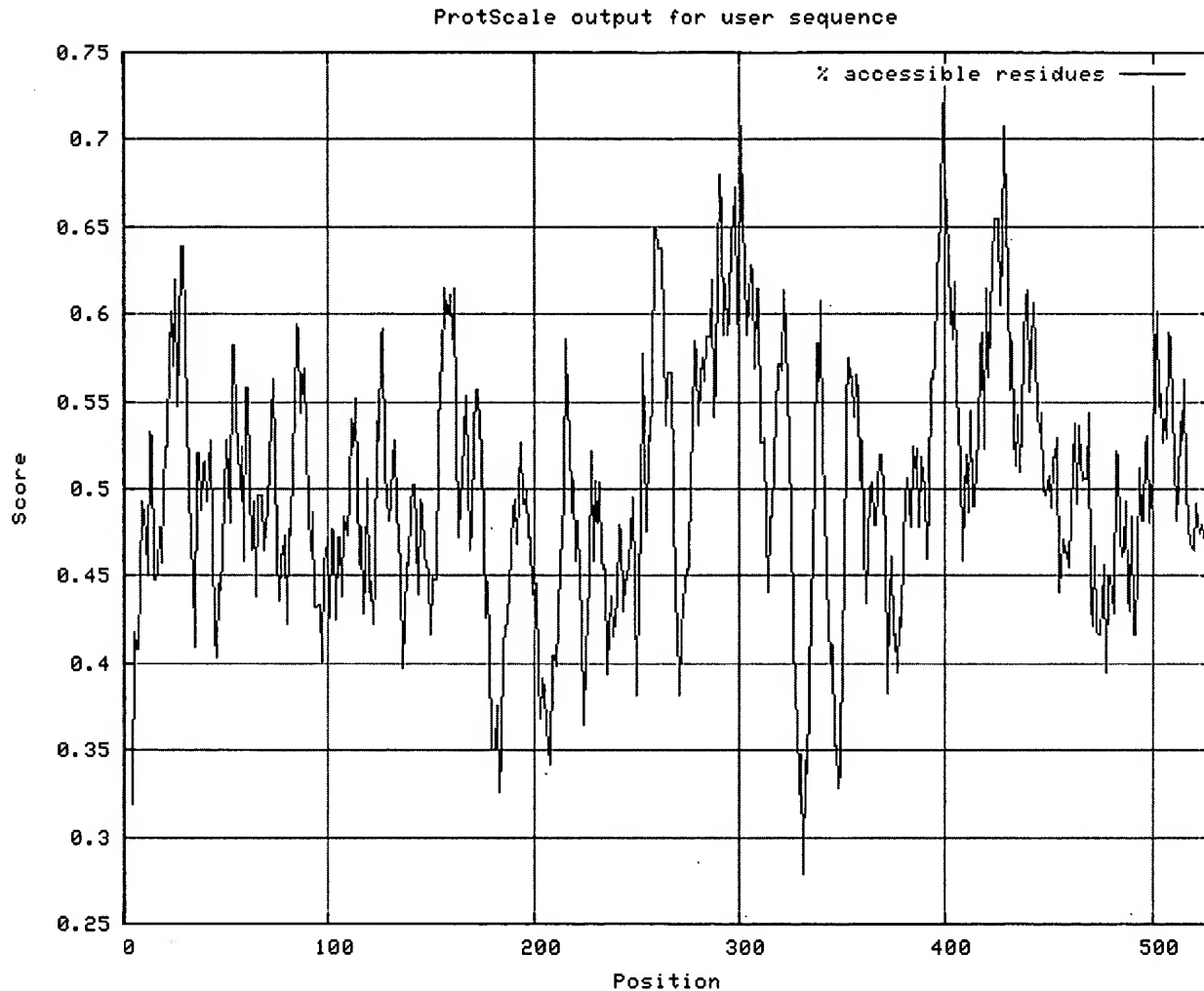


Figure 14a - 158P1D7 variant 1

Average Flexibility Profile

(Bhaskaran R., Ponnuswamy P.K., 1988.

Int. J. Pept. Protein Res. 32:242-255)

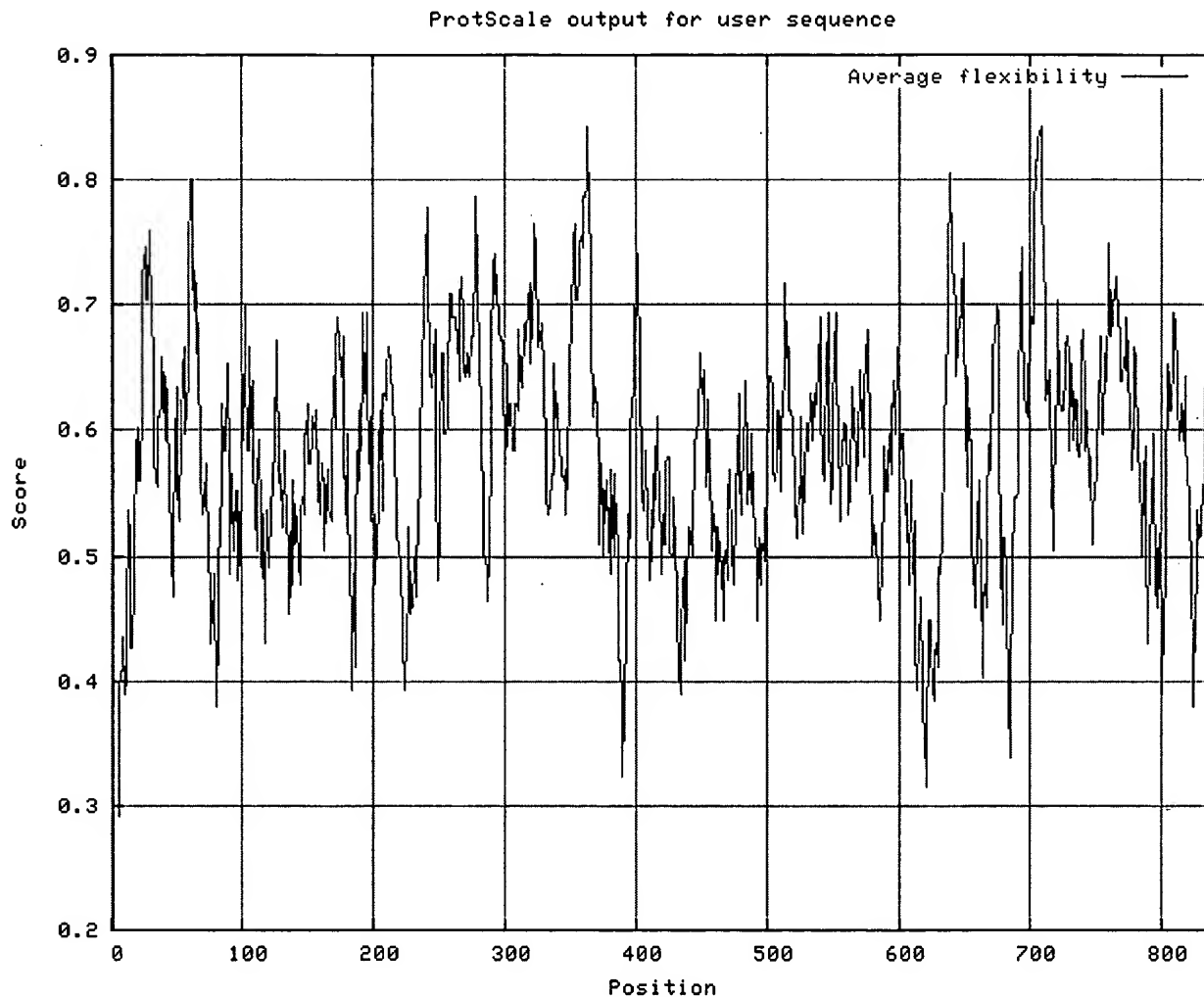


Figure 14B - 158P1D7 variant 3

Average Flexibility Profile

(Bhaskaran R., Ponnuswamy P.K., 1988.

Int. J. Pept. Protein Res. 32:242-255)

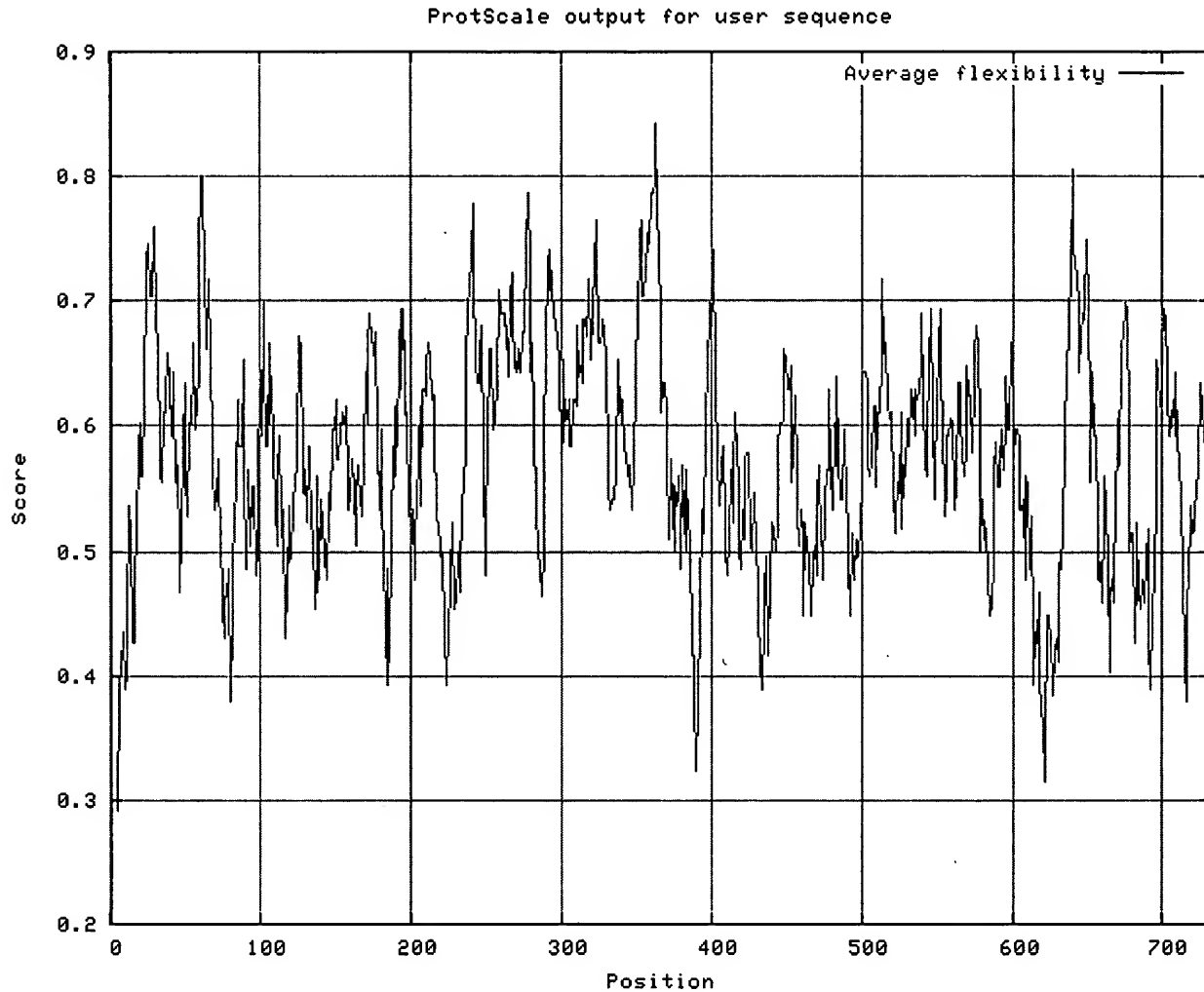


Figure 14c - 158P1D7 variant 4

Average Flexibility Profile

(Bhaskaran R., Ponnuswamy P.K., 1988.

Int. J. Pept. Protein Res. 32:242-255)

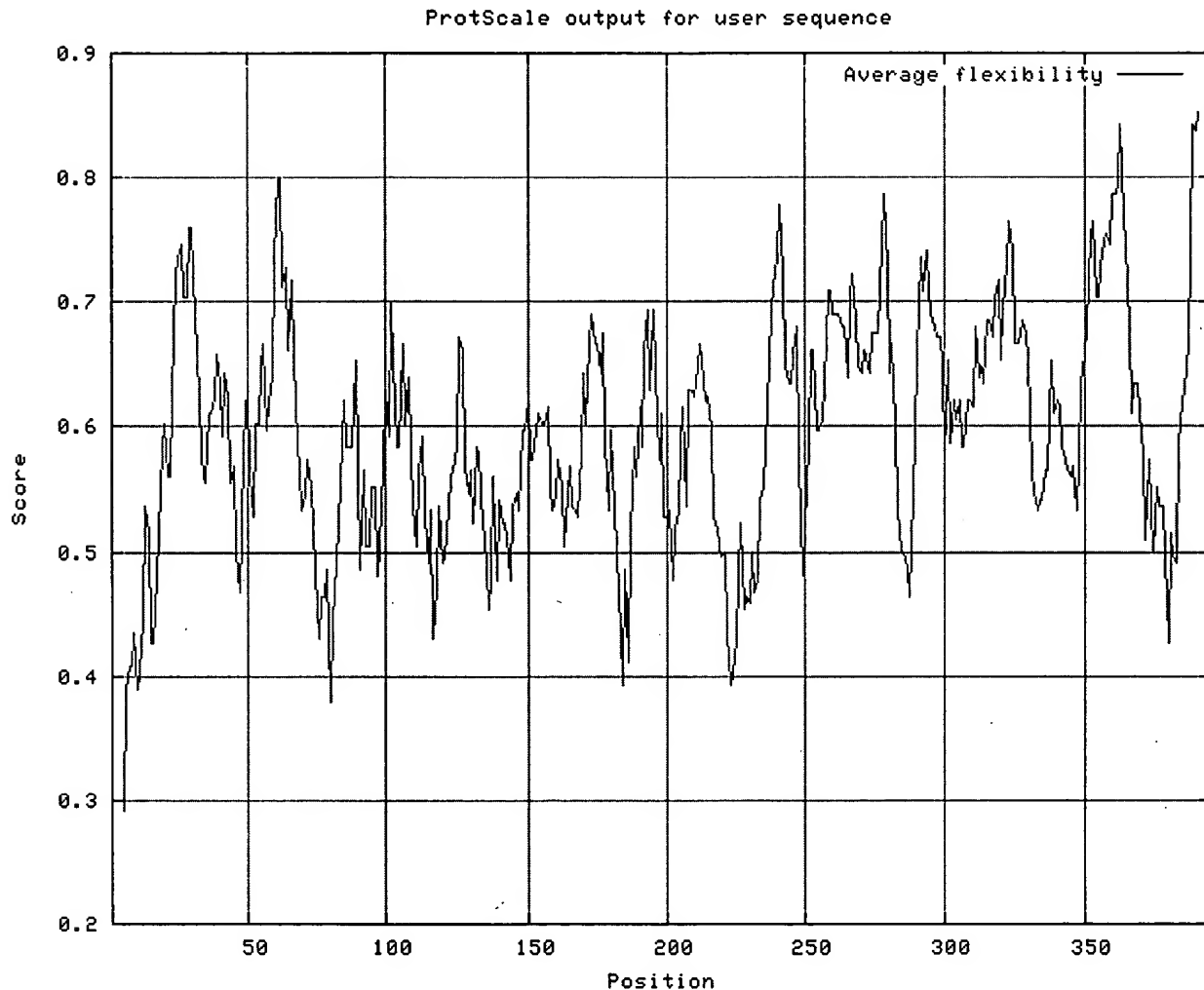


Figure 14d - 158P1D7 variant 6

Average Flexibility Profile

(Bhaskaran R., Ponnuswamy P.K., 1988.

Int. J. Pept. Protein Res. 32:242-255)

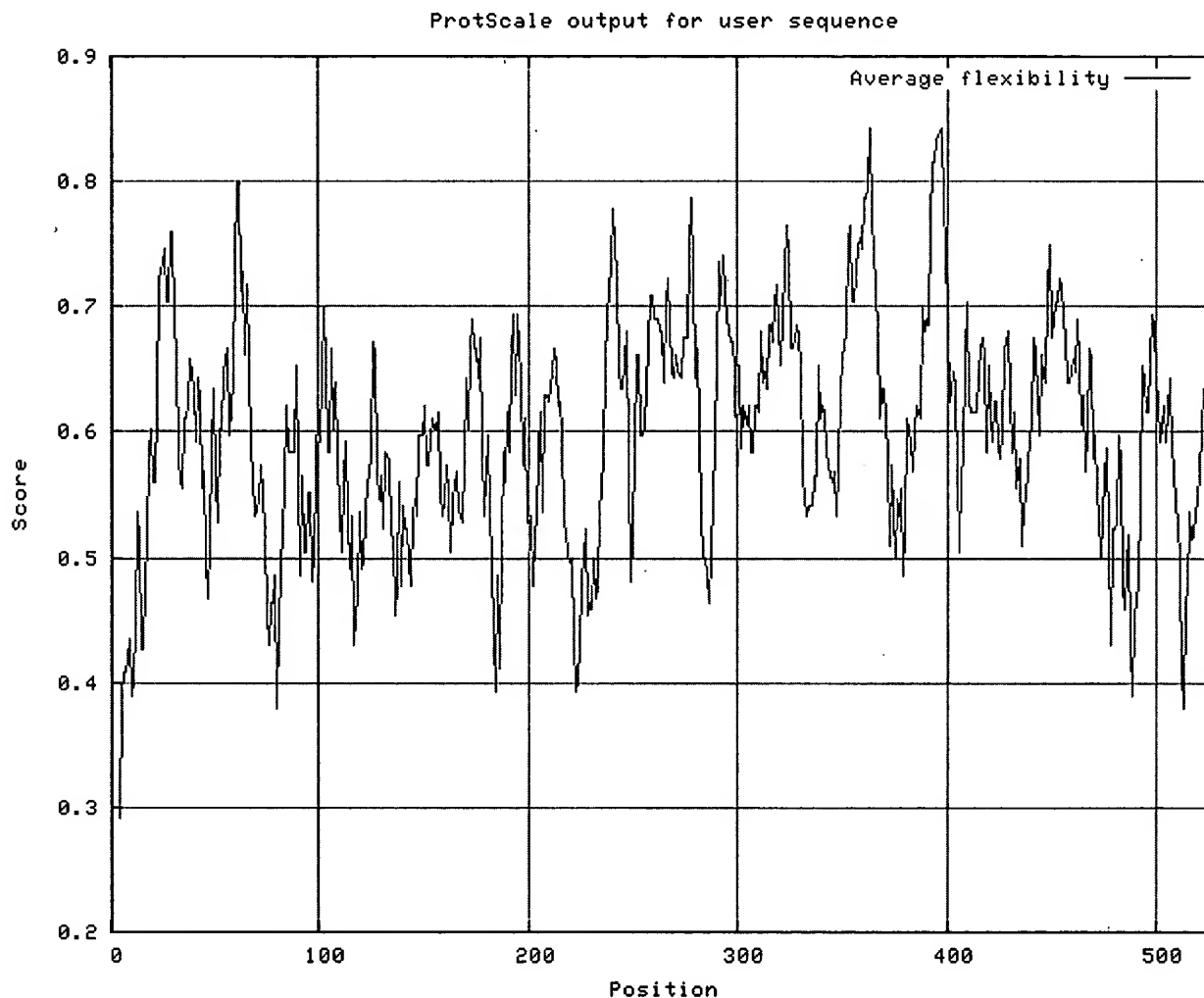


Figure 15a - 158P1D7
variant 1 Beta-turn Profile
(Deleage, G., Roux B. 1987.
Protein Engineering 1:289-294)

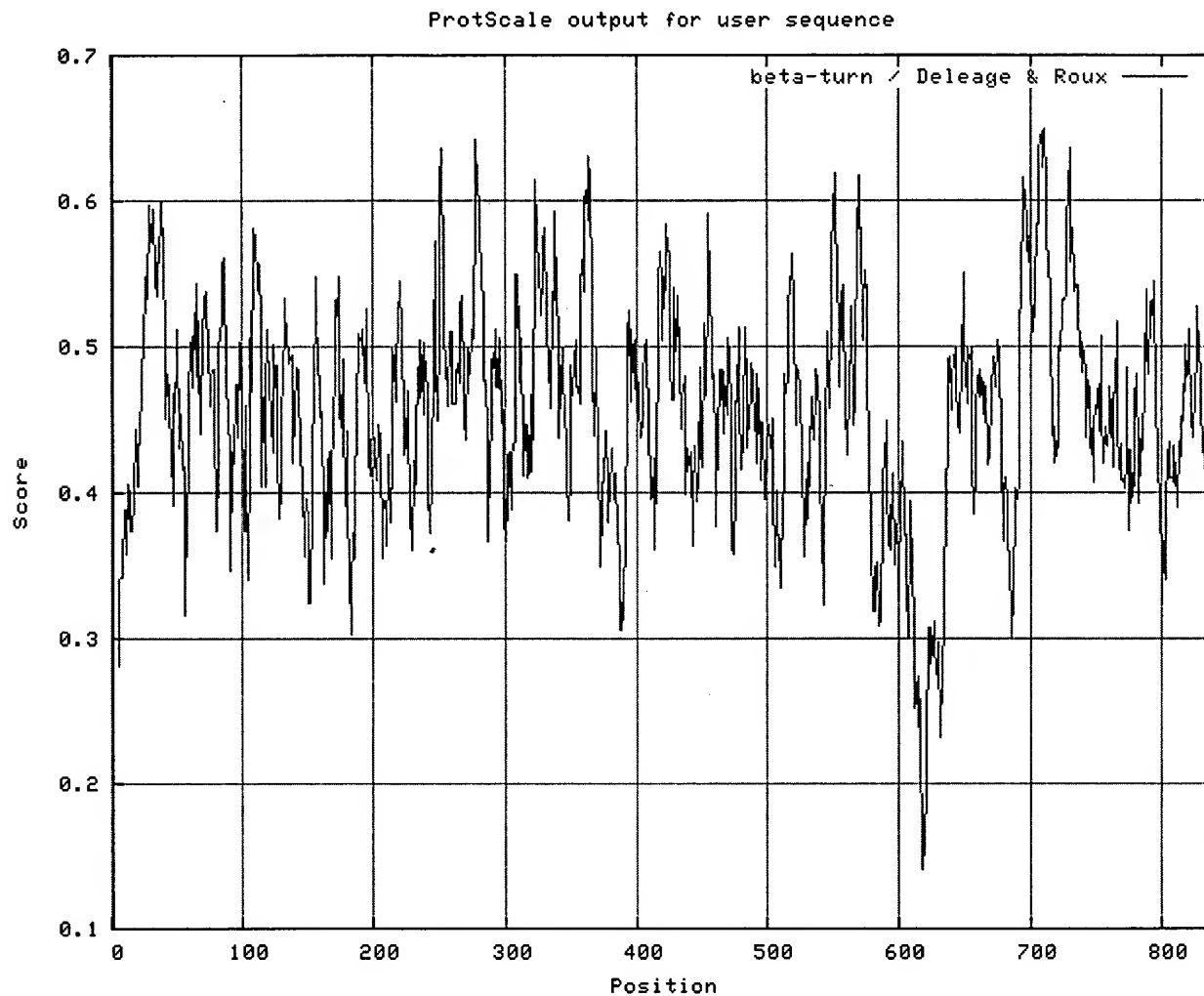


Figure 15b - 158P1D7 variant 3

Beta-turn Profile

(Deleage, G., Roux B. 1987.
Protein Engineering 1:289-294)

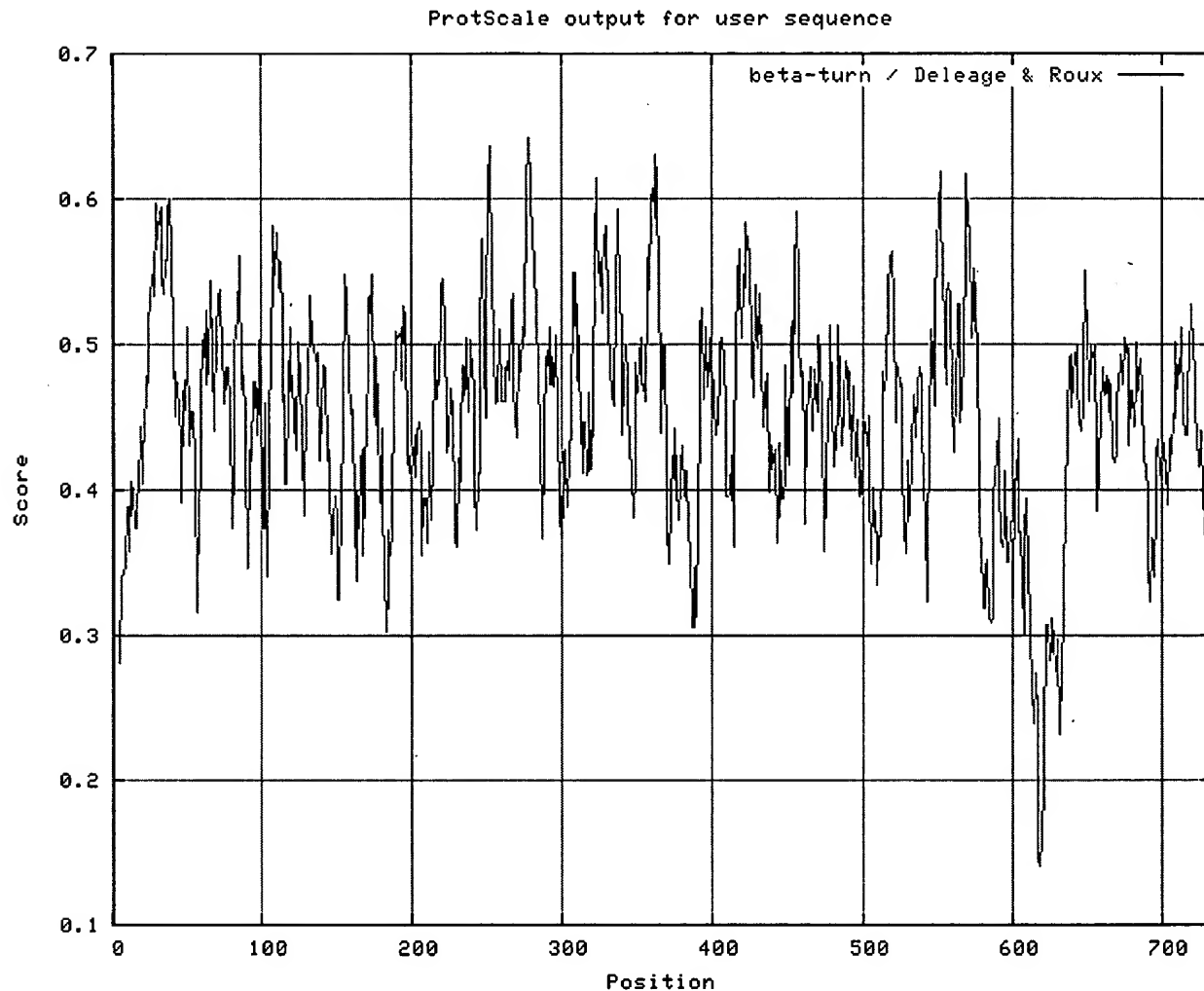


Figure 15c - 158P1D7 variant 4

Beta-turn Profile

(Deleage, G., Roux B. 1987.
Protein Engineering 1:289-294)

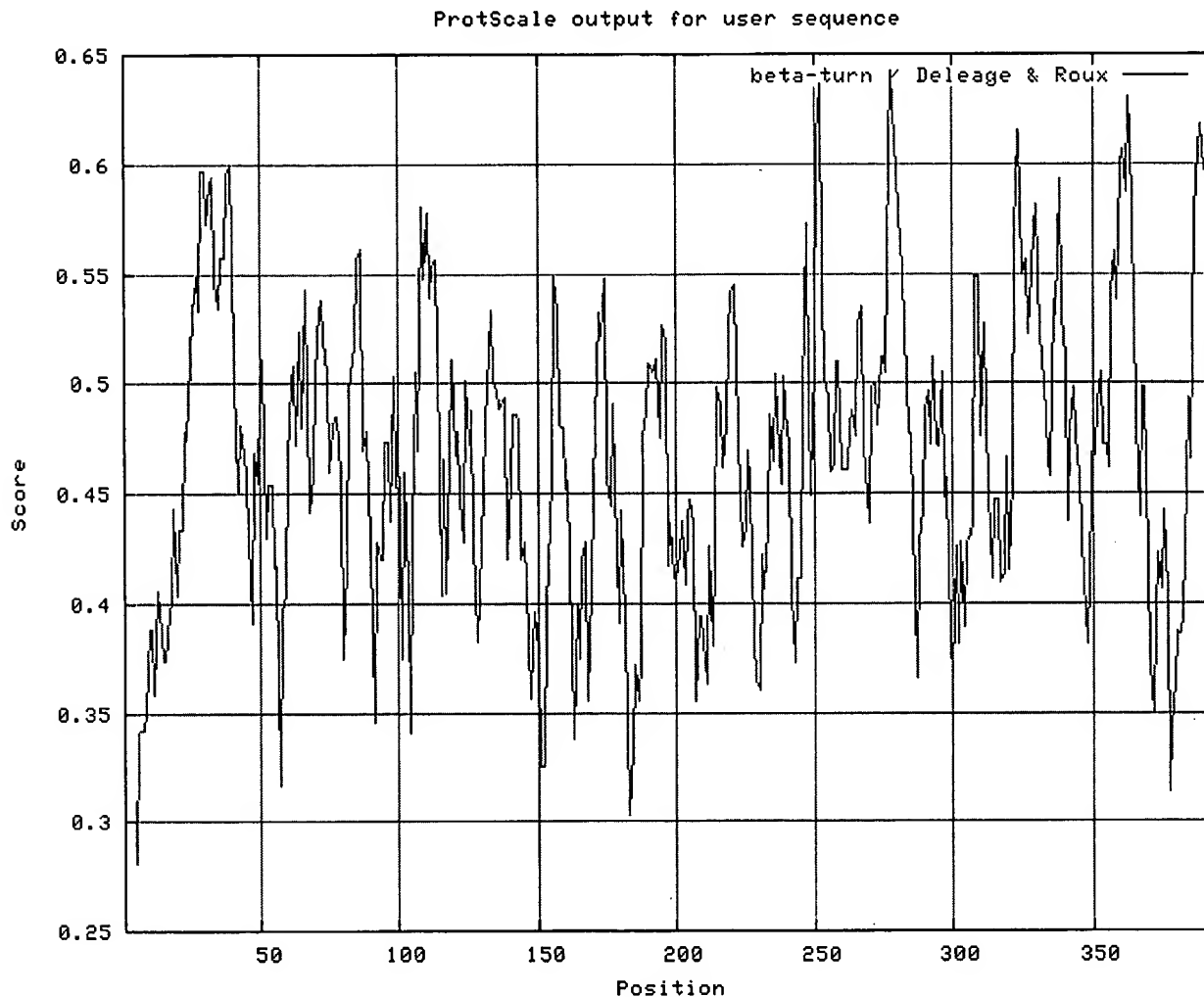


Figure 15d - 158P1D7 variant 6

Beta-turn Profile

(Deleage, G., Roux B. 1987.
Protein Engineering 1:289-294)

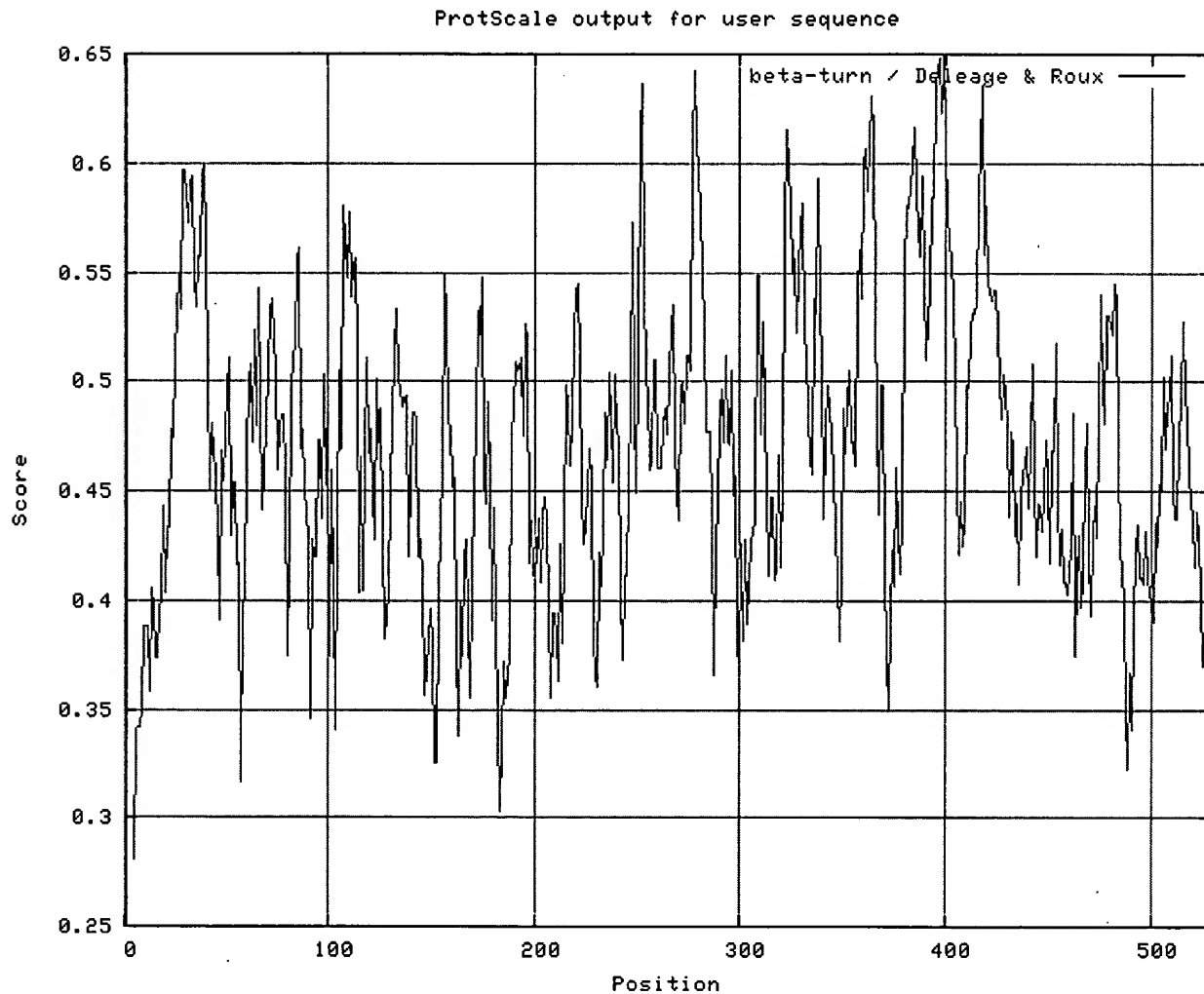


Fig 16A
Secondary structure prediction of 158P1D7 variant 1

	10	20	30	40	50	60	70	80
MKLWIHLFYSSLLACISLHSQTPVLSRSGCDSLCNCCEKDGTMLINCEAKGIKMVSEISVPPSRPFQLSLLNGLTMLH cchhhhhhhhhhecc TNDPSGLTNAISIHGLFNNIADIEIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENLFLQADNNFITVIEPSAFSKLN cccccchhhheeeecchhhhhhhhhcchhhhhhecc RLKVLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPYVGFLIEHIGRIILDQLQLEDNKWACNDLLQLKTWLENMPPOS ceeeeccccchhccccchhecc IIGDVVCSNPPFFKGSILSRLKKESICPTPPVYEEHEDPSGSLHLAATSSINDSRMSTKTTTSSILKLPKAPGLIPYITKP eeeccccccccchhhhhchcc STQLPGPYCPIPCNCKVLSPSGLLIHCQERNIESLSDLRPPQNPRKLILAGNIHSLMKSDLVEYFTLEMLHLGNRNRIE ccc VLEEGSPMNLTRLQKLYLNGNHLTKLSKGMFLGLHNLEYLYLEYNAIKEILPGTFNPMPLKVLYLNNLLQVLPPPHIFS eeeccchhhhhhhhhccccchhhchhh GVPLTKVNLKTNQFTHLPVSNILDDDLLLTQIDLEDNPWDCSDLVGLQQWIKLSKNTVTDDILCTSPGHLDKKELKAL cccccccccccccccccchhhhhhhceeecc NSEILCPGLVNNPSMPTQTSYLMVTTTATTNTADTILRSLTDAVPLSVLILGLLIMFITIVFCAAGIVVLVHRRRRRYK cchhhhhhhhhcchhhhhhhhhhhhhhhhhhhhhhhhhhh KKQVDEQMRDNSPVHLQYSMYGHKTHHTTERPSASLYEQHMVSPMVHVYRSPSFGPKHLEEEERNEKEGSDAKHLQRS hhchhhhhcc LLEQENHSPLTGSNMKYKTTNQSTEFSLFQDASSLYRNILEKERELQQLGITEYLRKNIAQLQPDMEAHYPGAHEELKLM hhhccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh ETLMYSRPRKVLVEQTKNEYFELKANLHAEPDYLEVLEQQT	Alpha helix (h): 35.32% Extended strand (e): 15.93% Random coil (c): 48.75%							

Secondary structure prediction of 158P1D7 variant 3

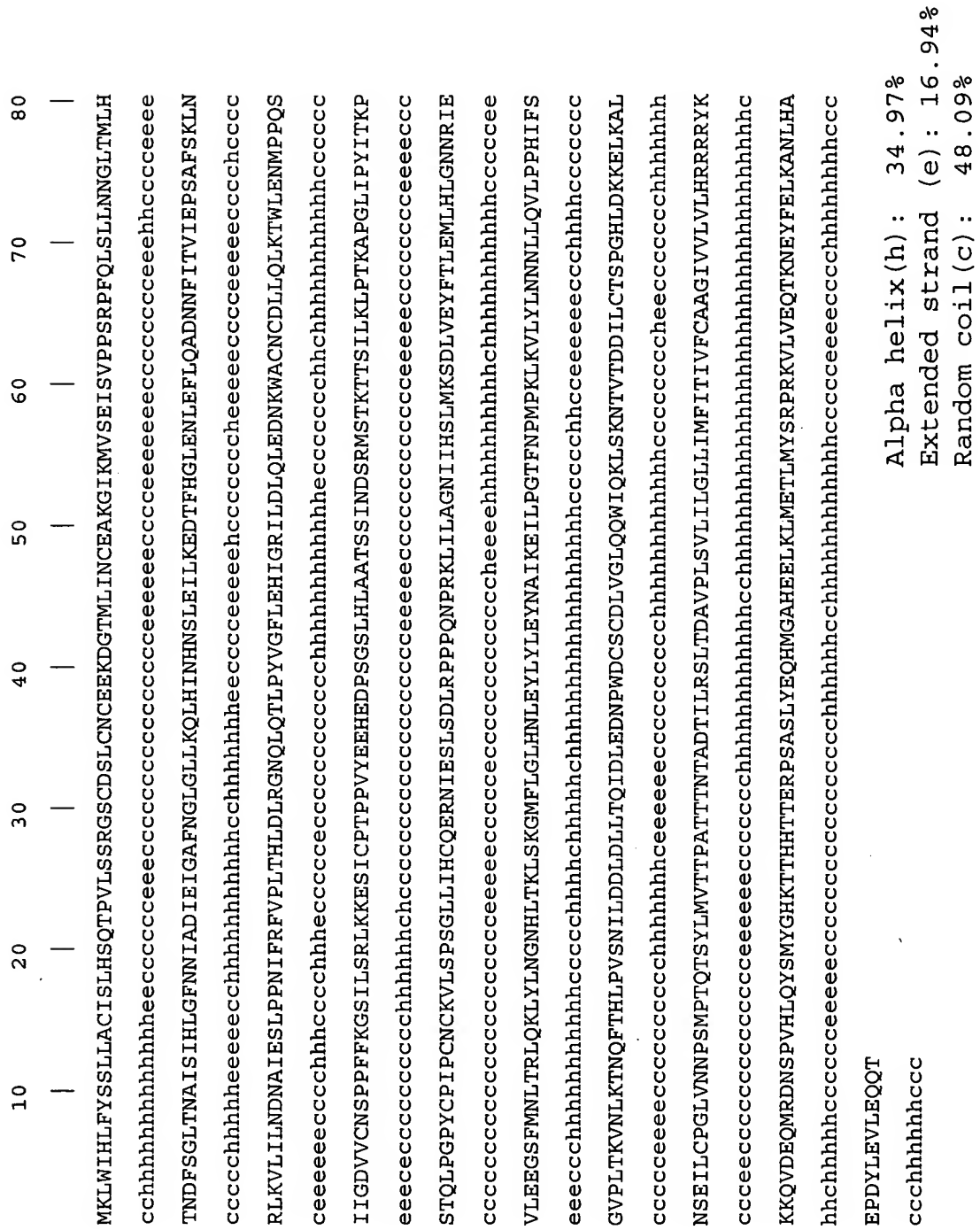
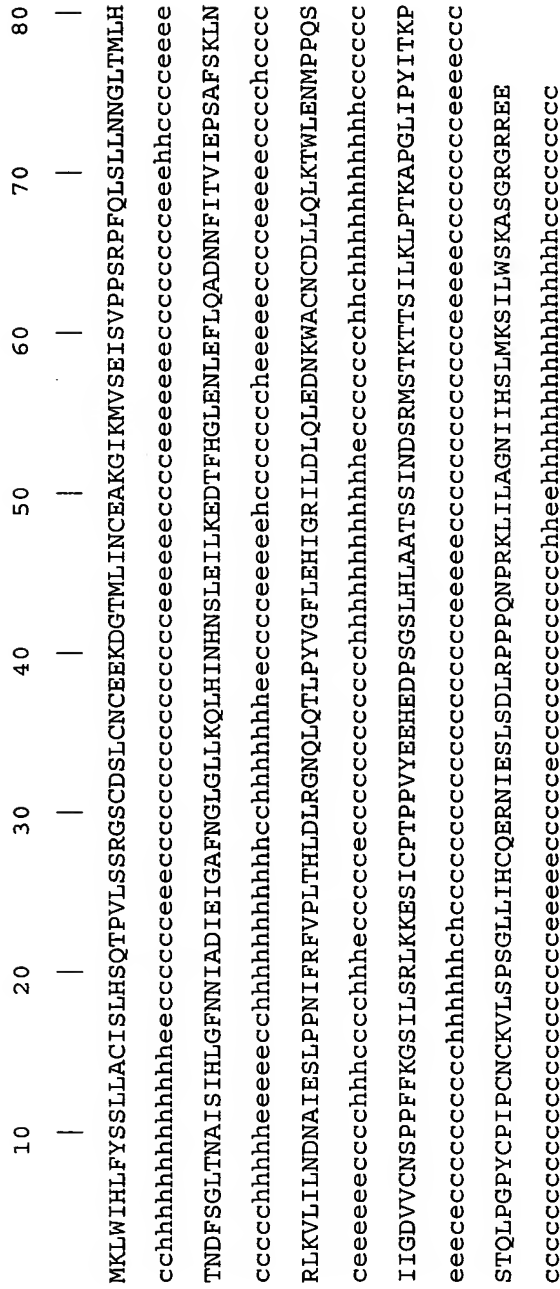


Fig 16C
Secondary structure prediction of 158P1D7 variant 4



Alpha helix(h): 24.56%
Extended strand (e): 20.76%
Random coil(c): 54.68%

Fig 16D
Secondary structure prediction of 158P1D7 variant 6

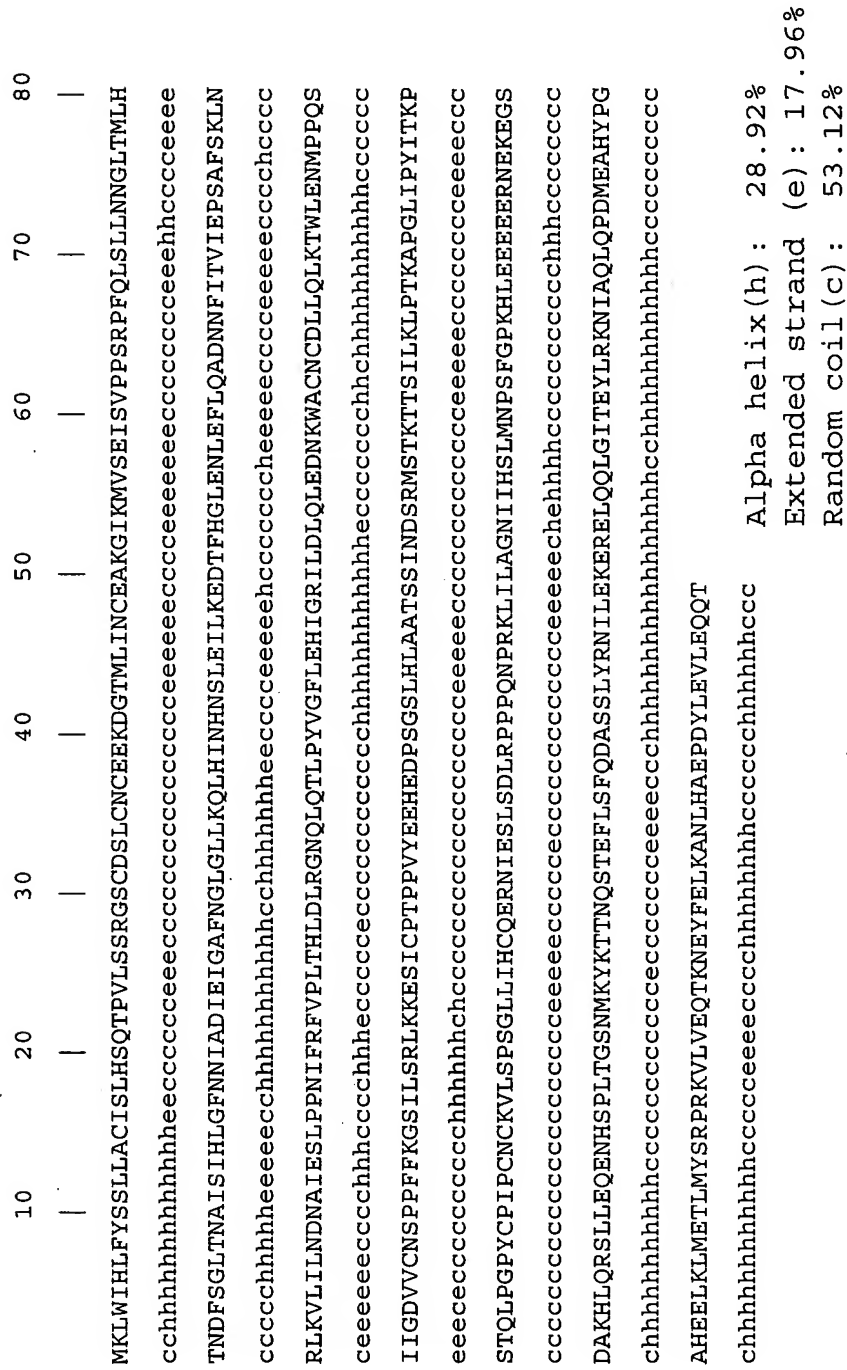
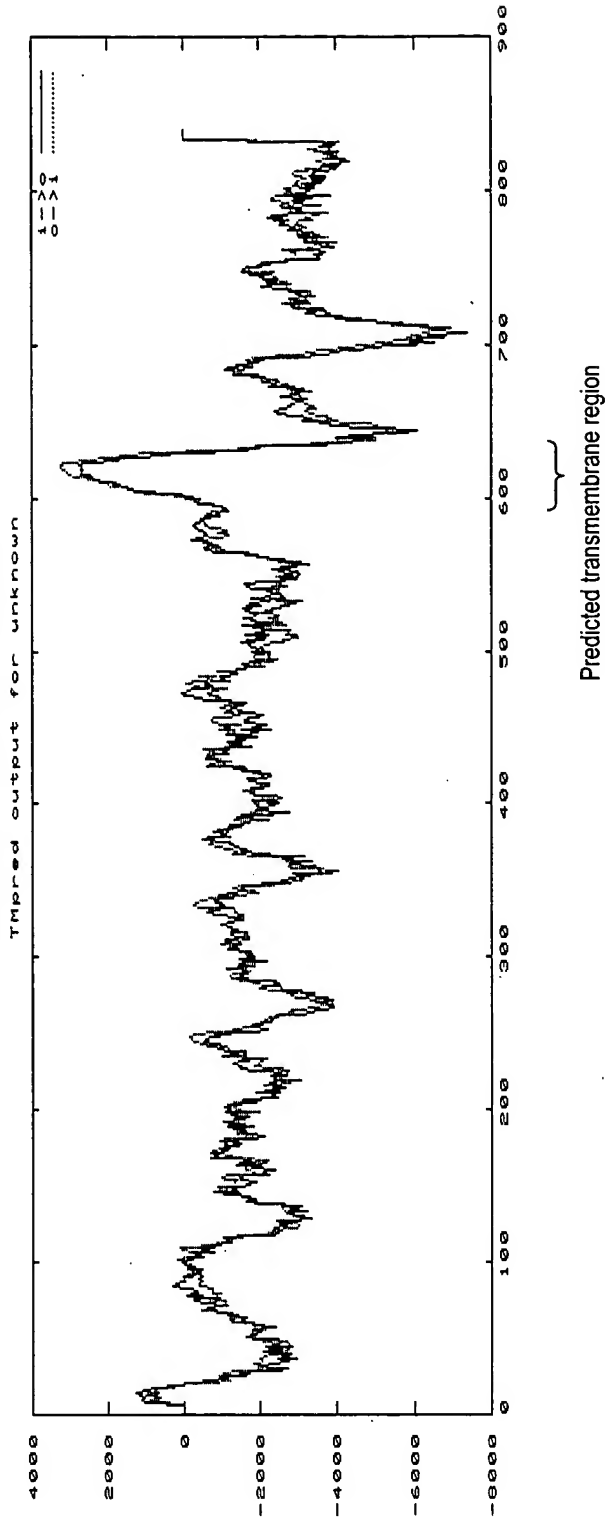


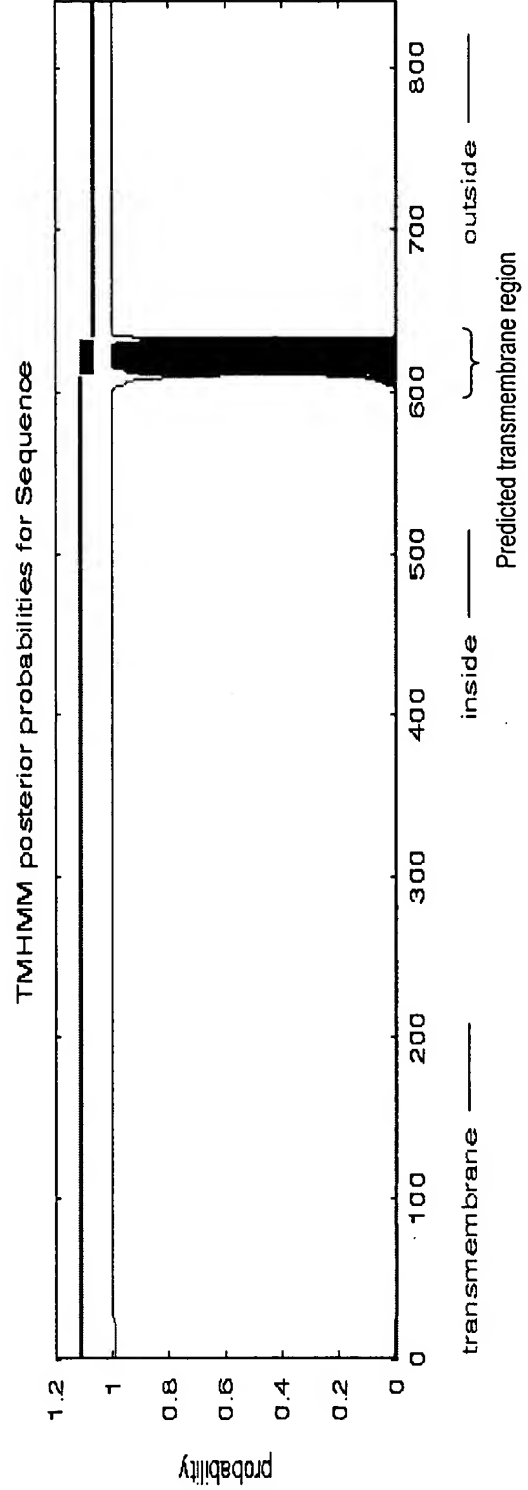
Fig 16E

Transmembrane prediction for 158P1D7 variant 1



1 transmembrane
domain
predicted

Fig 16F



1 transmembrane
domain
predicted

Transmembrane prediction for 158P1D7 variant 3

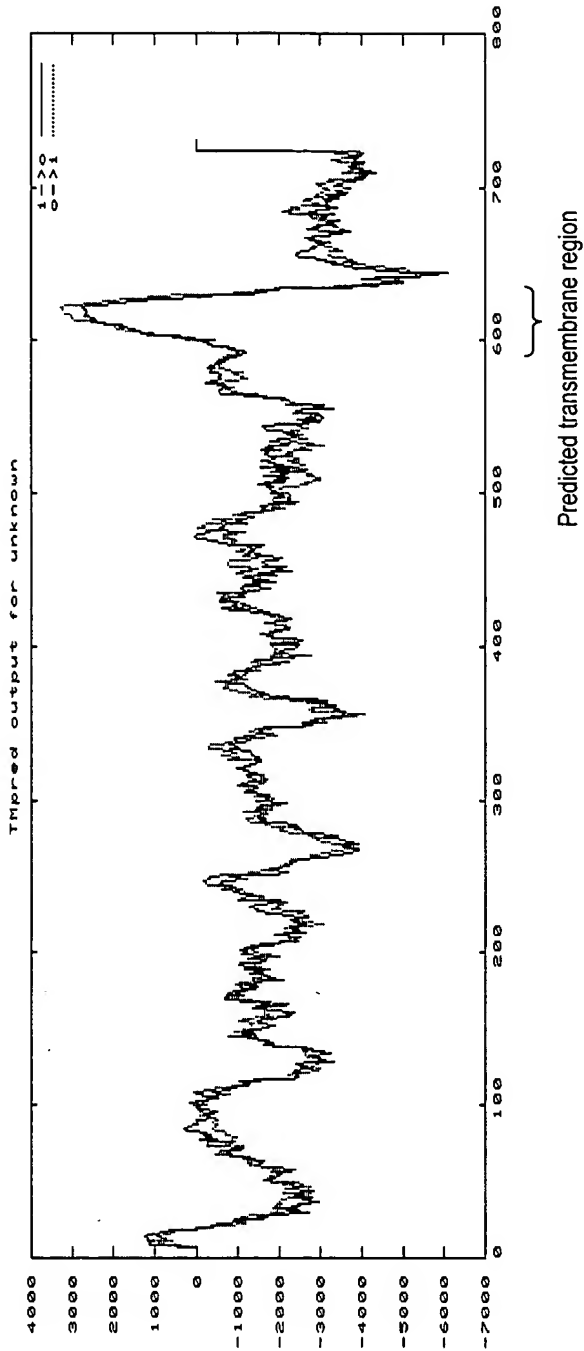
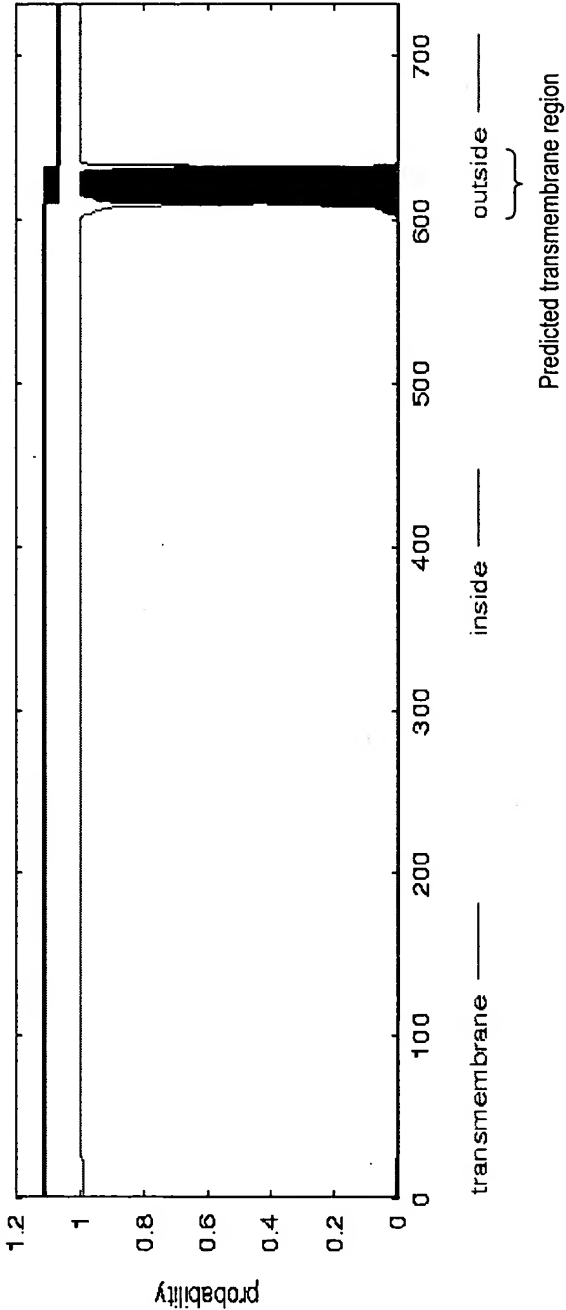


Fig 16G

1 transmembrane
domain
predicted

Fig 16H



1 transmembrane
domain
predicted

Fig 16I

Transmembrane prediction for 158P1D7 variant 4

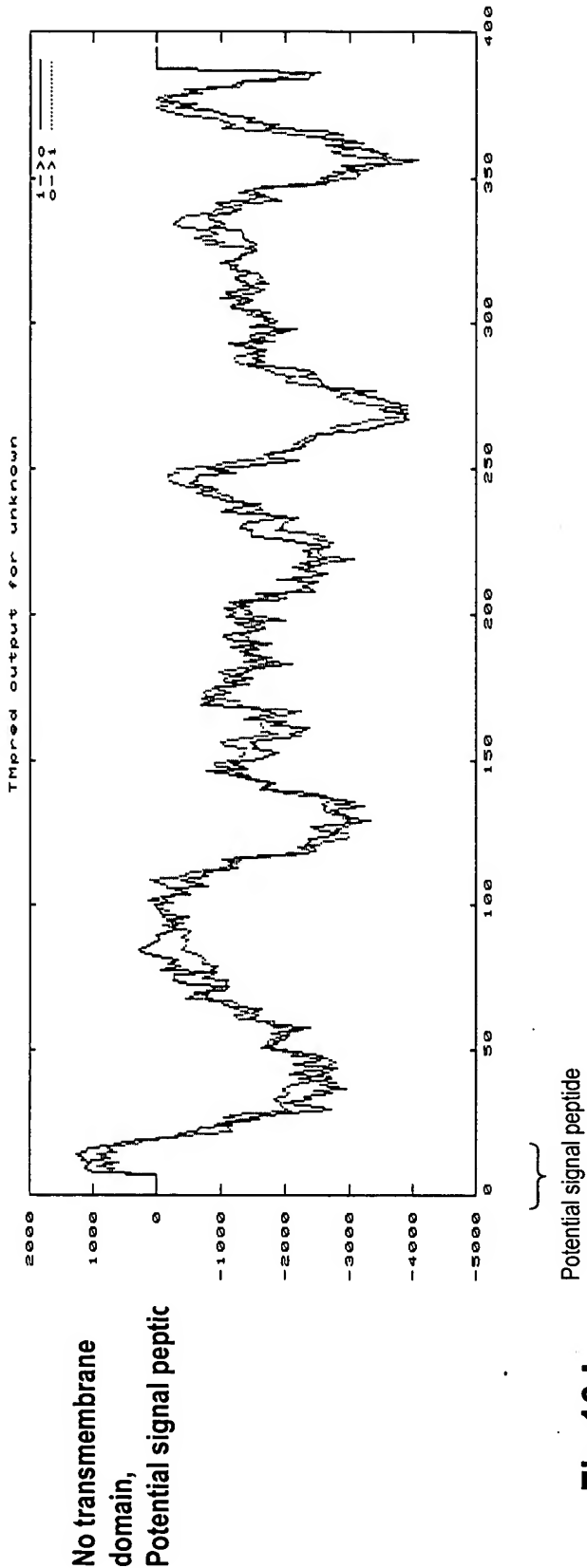


Fig 16J

TMHMM posterior probabilities for Sequence

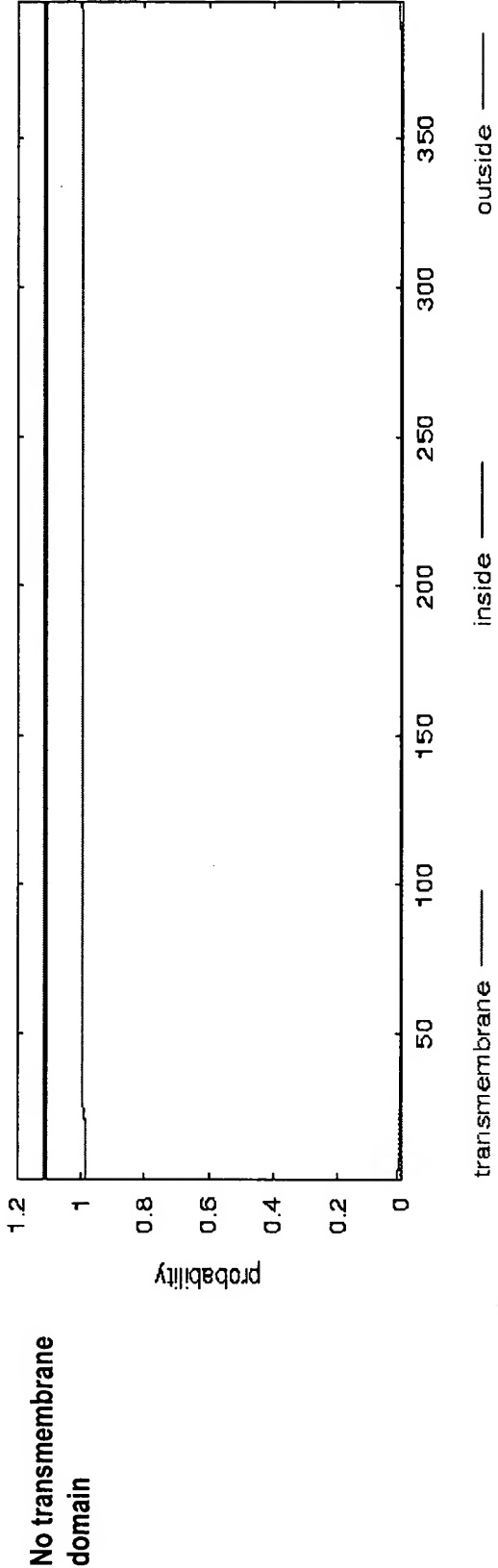
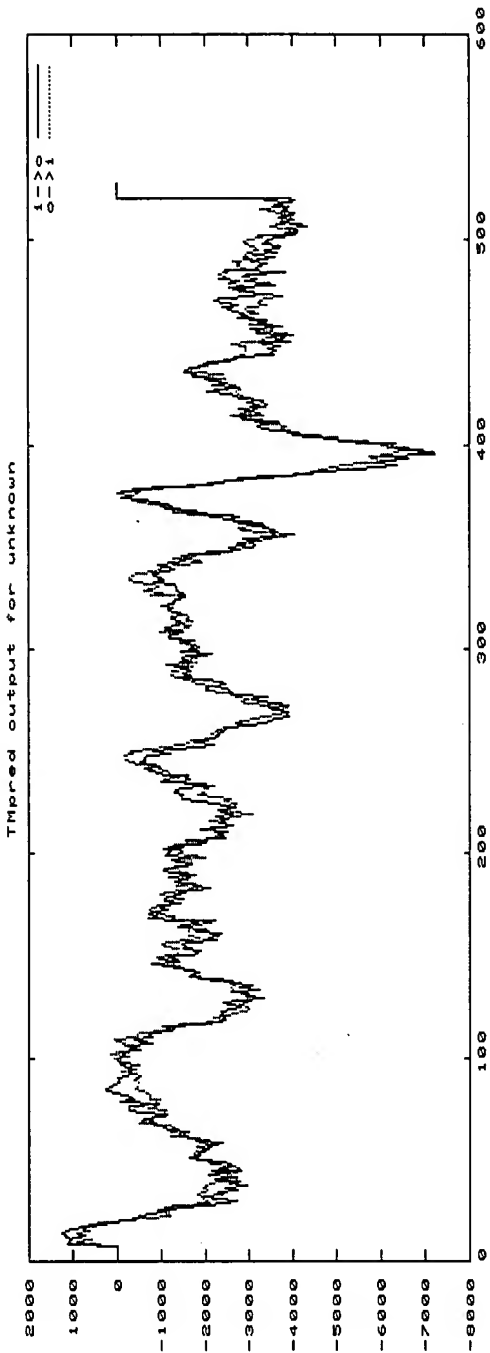


Fig 16K

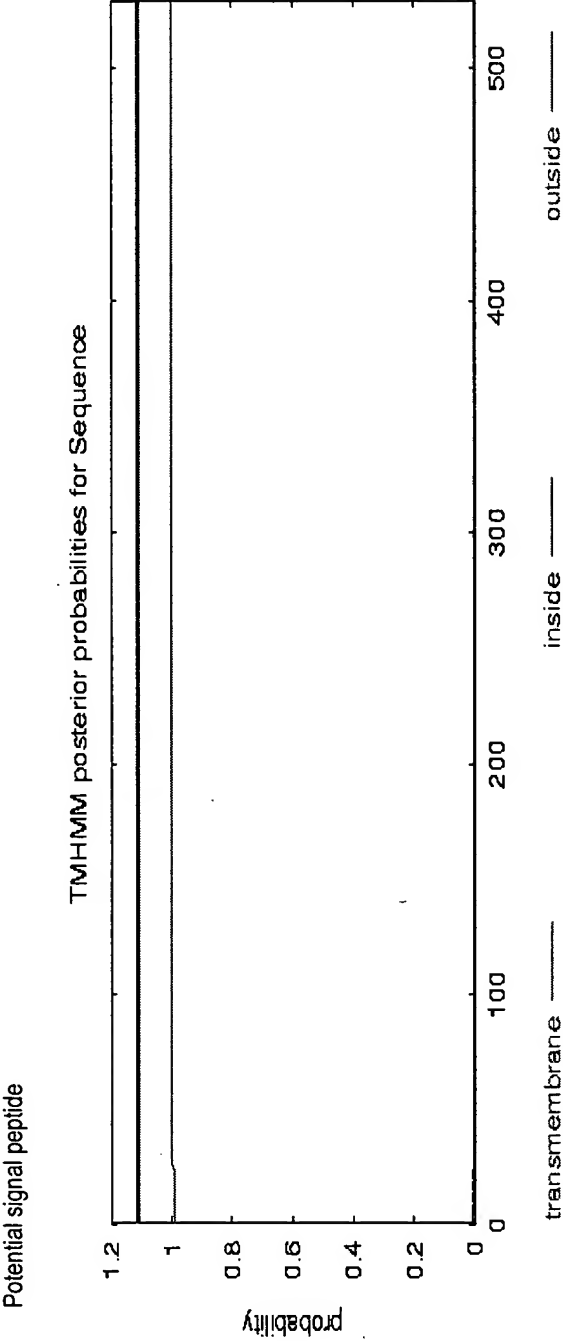
Transmembrane prediction for 158P1D7 variant 6



No transmembrane
domain,
Potential signal peptide

Fig 16L

TMHMM posterior probabilities for Sequence



No transmembrane
domain

Figure 17



Figure 18

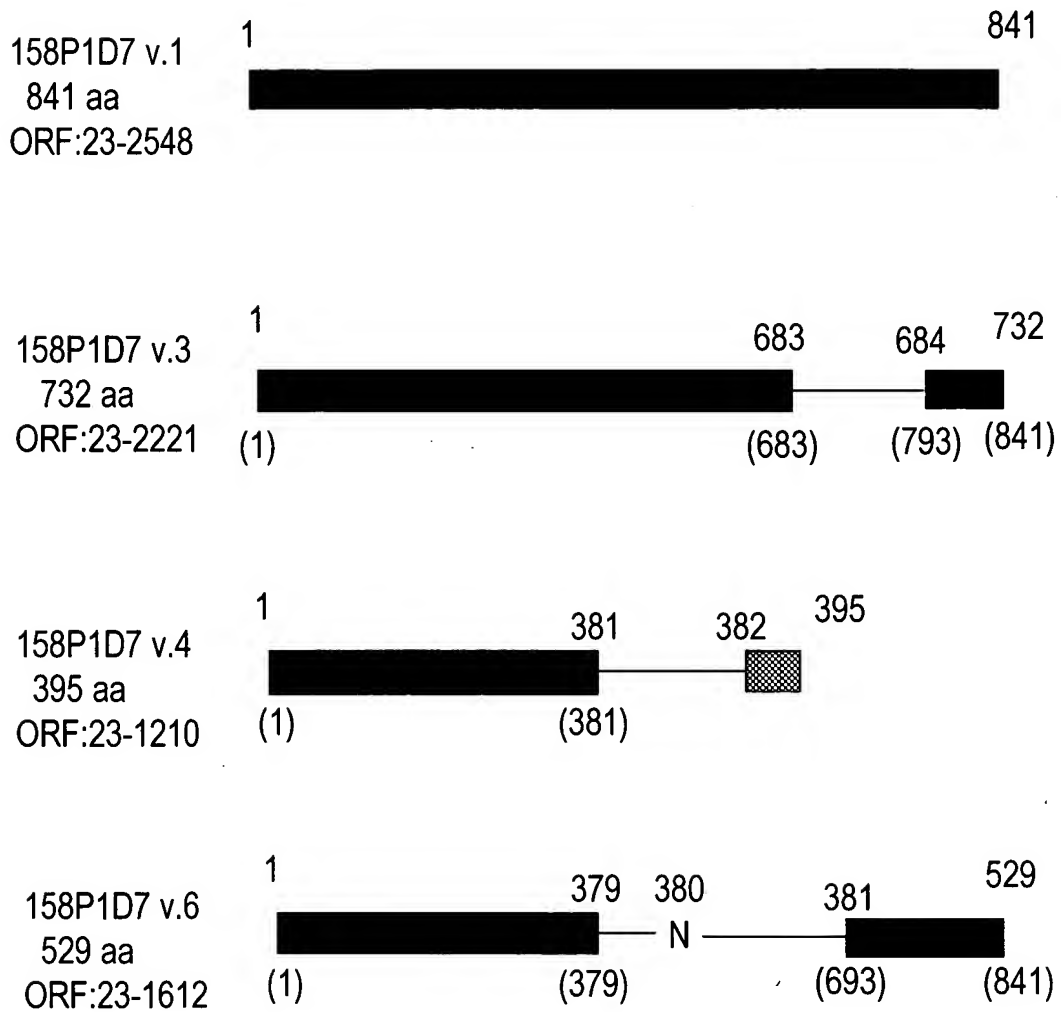


Figure 19

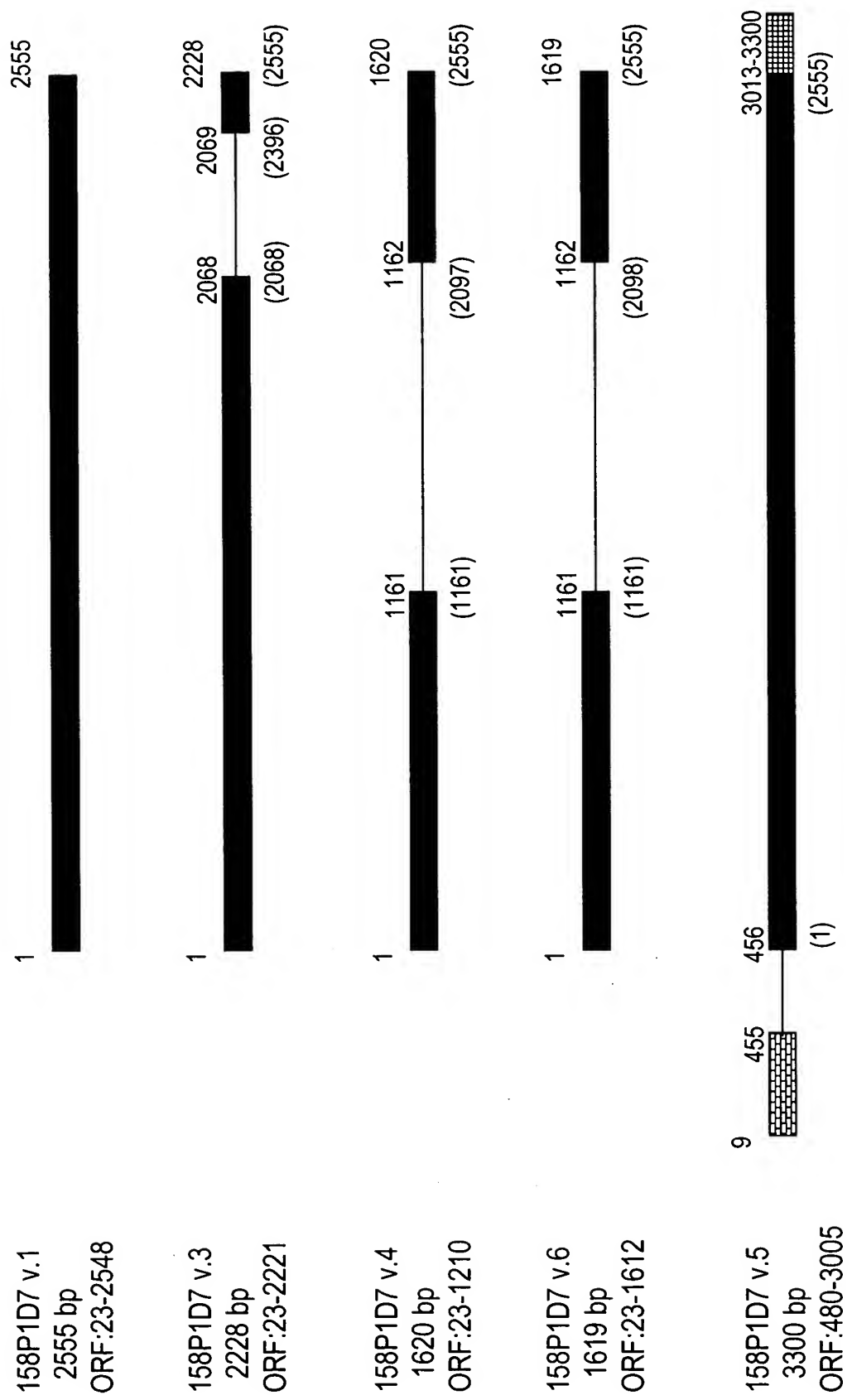


Figure 20 158P1D7 Expression in Melanoma

1 2



1. Normal skin cell line - Detroit-551
2. Melanoma cancer cell line -- A375

**Figure 21 158P1D7 Expression in Cervical
 Cancer Patient Specimens**

Panel#	Patient ID#	Diagnosis	Grade	Stage	Cervix CA
1	Normal Cervix	(Ambion)			
2	HeLa	Cell Line			
3	USA-00281-D01	Intraepithelial neoplasia	2-3	T3AN0MX	
4	VNM-00266	AdenoCA	1	IIA	
5	VNM-00376	AdenoCA	1	IIA	
6	IND-00396	Mucinous AdenoCA	2	IIB	
7	A0098	Adenosquamous	2B	T2bNXM0	

No expression

Positive expression



Figure 22: Detection of AGS15 protein in recombinant cells
 with monoclonal antibodies

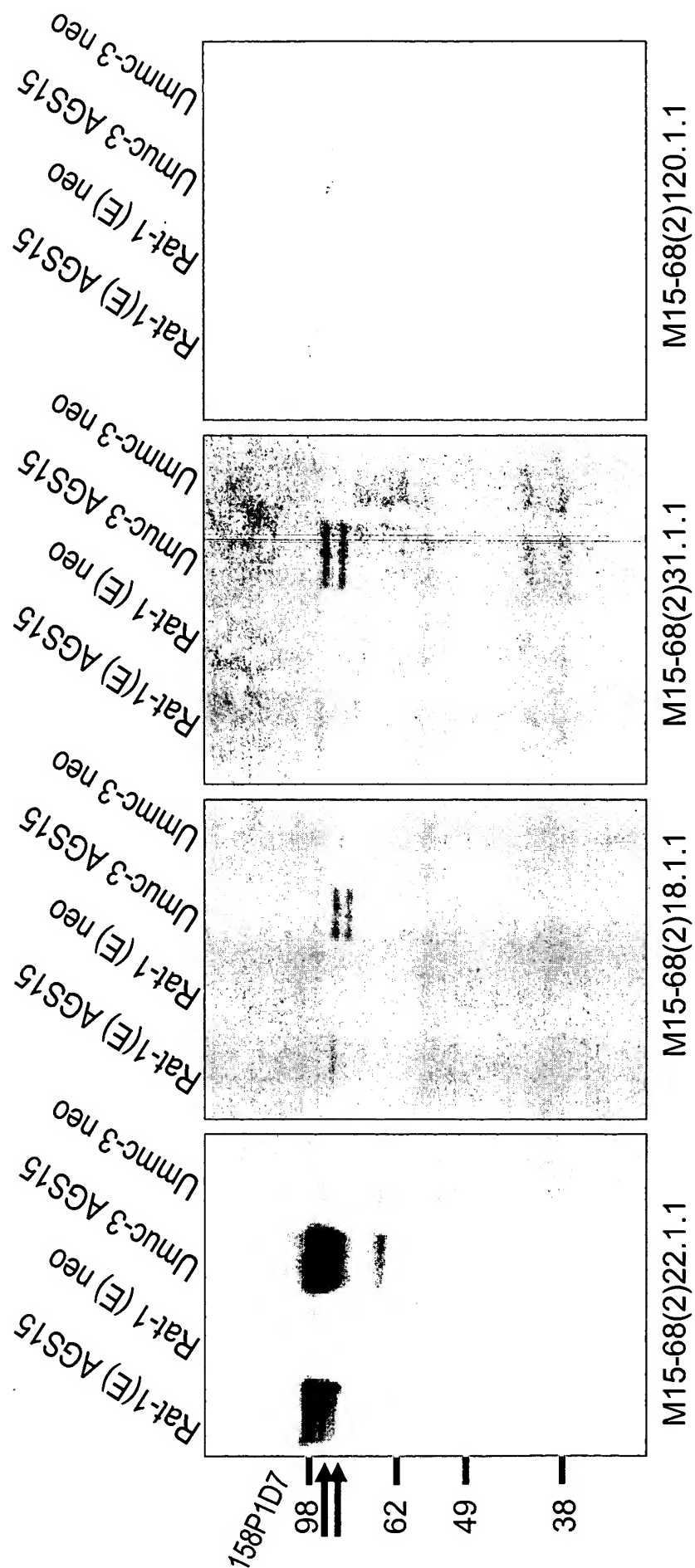


Figure 23: Surface staining of AGS15-expressing 293T and UMUC cells
 with anti-AGS15 monoclonal antibodies

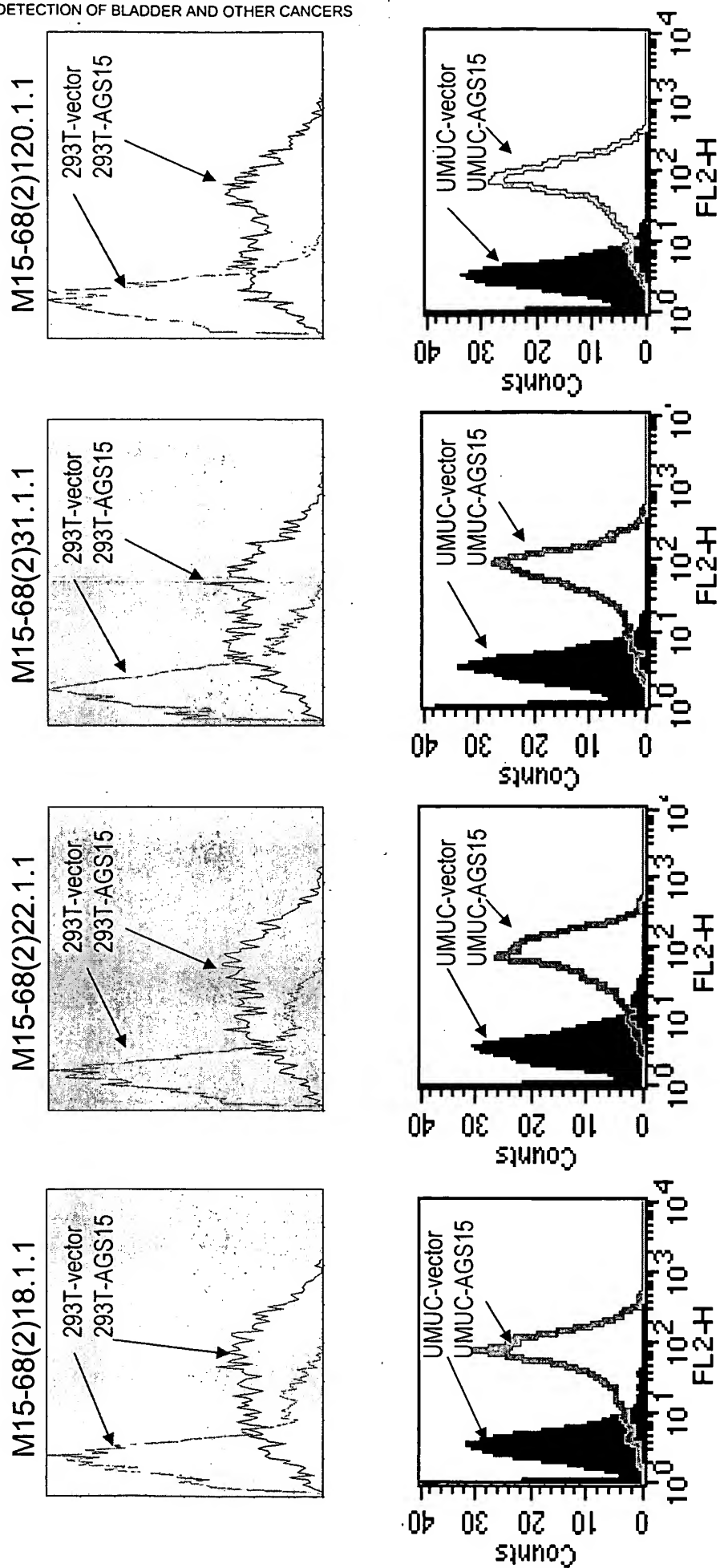


Figure 24: Surface staining of endogenous AGS15-expressing LAPC9 prostate cancer
and UGB1 bladder cancer xenograft cells with MAb M15-68(2)22.1.1

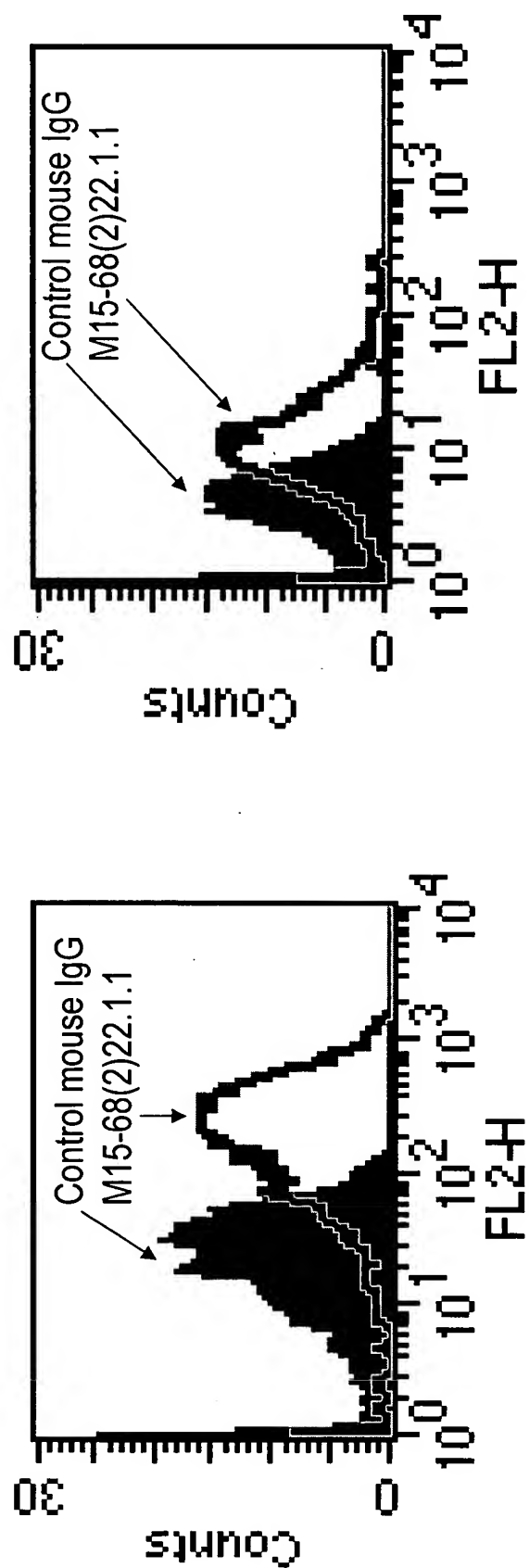


Figure 25: Monoclonal antibody-mediated internalization of endogenous surface 158P1D7 in NCI-H146 small cell lung cancer cells

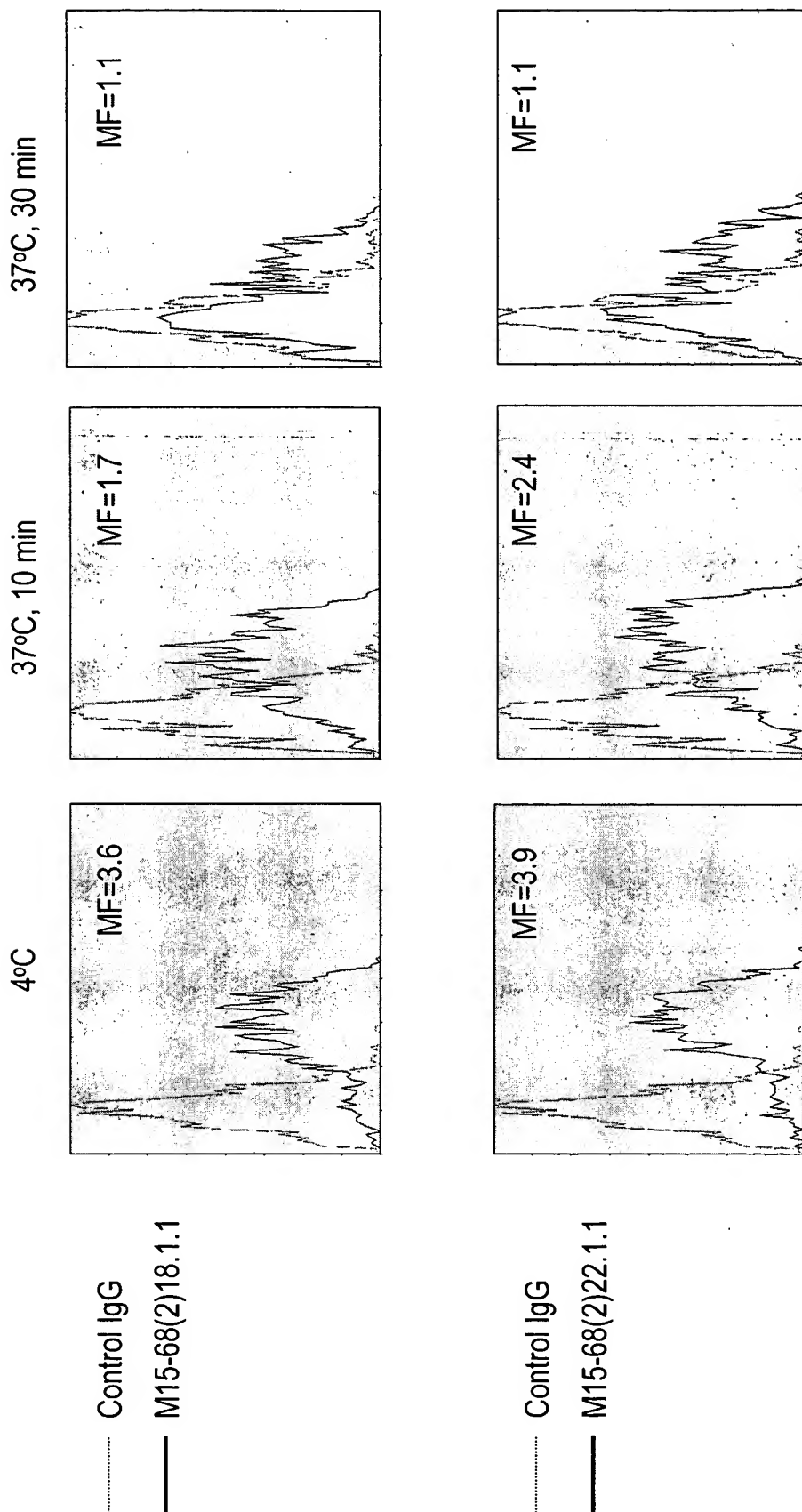


Figure 25 Cont.

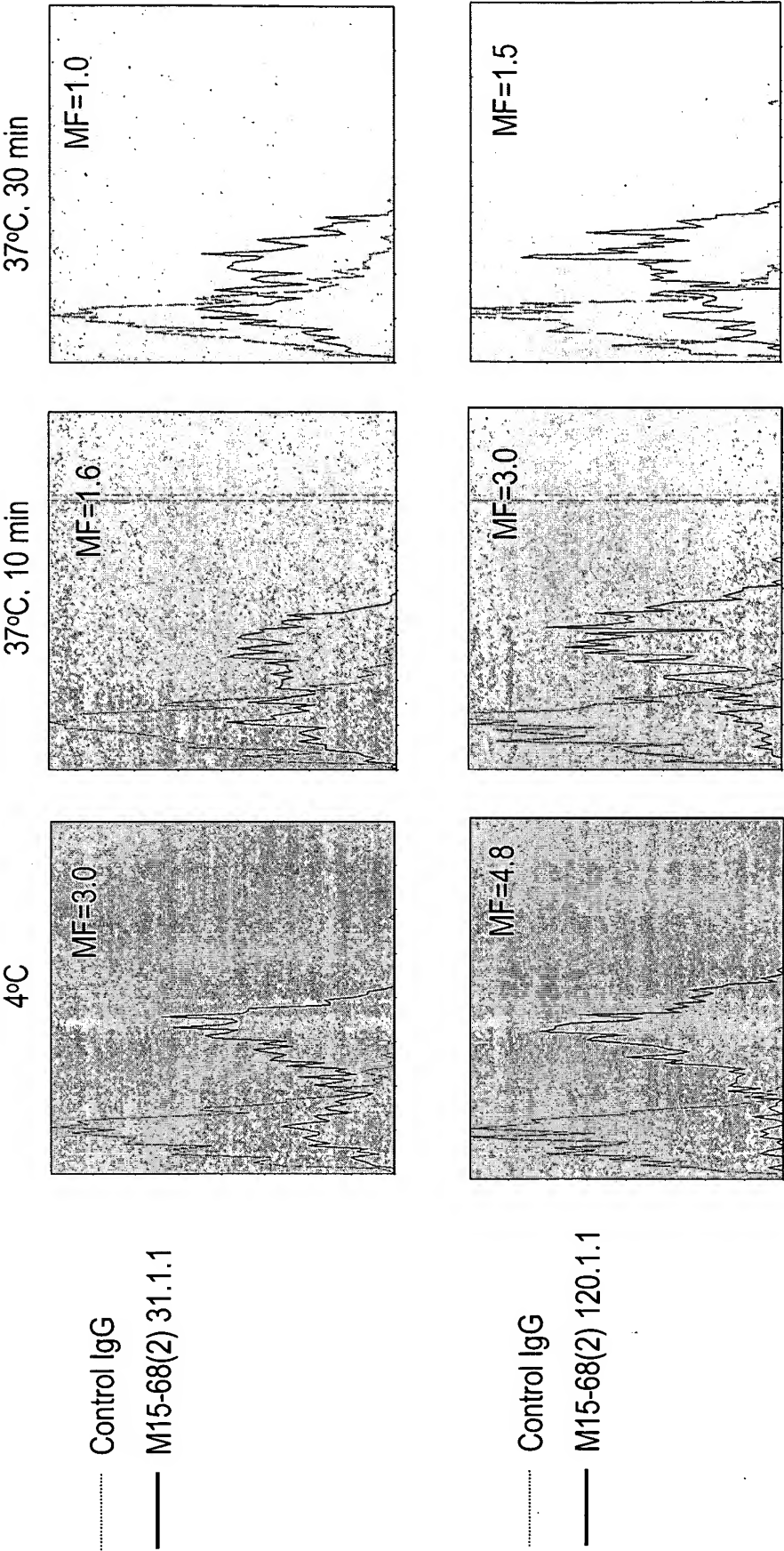
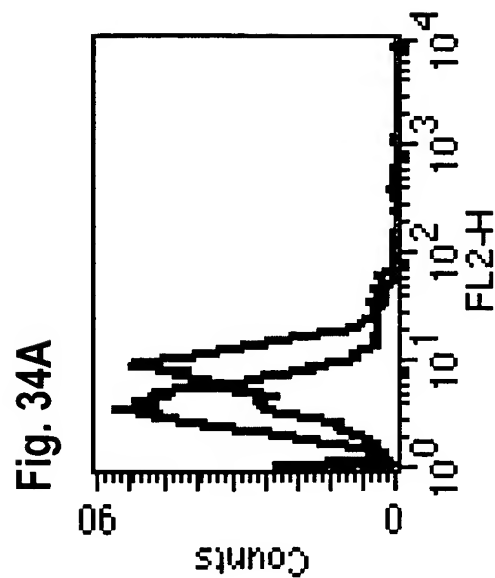


Figure 26: Binding of the 158P1D7 extracellular domain to human umbilical vein endothelial cells (HUVEC)



Key	Name	Parameter	Gate
—	HUVEC No ECD / anti-158P1D7-PE	FL2-H	G1
—	HUVEC 158P1D7 ECD / anti-158P1D7-PE	FL2-H	G1

2.88% vs 6.53% gated

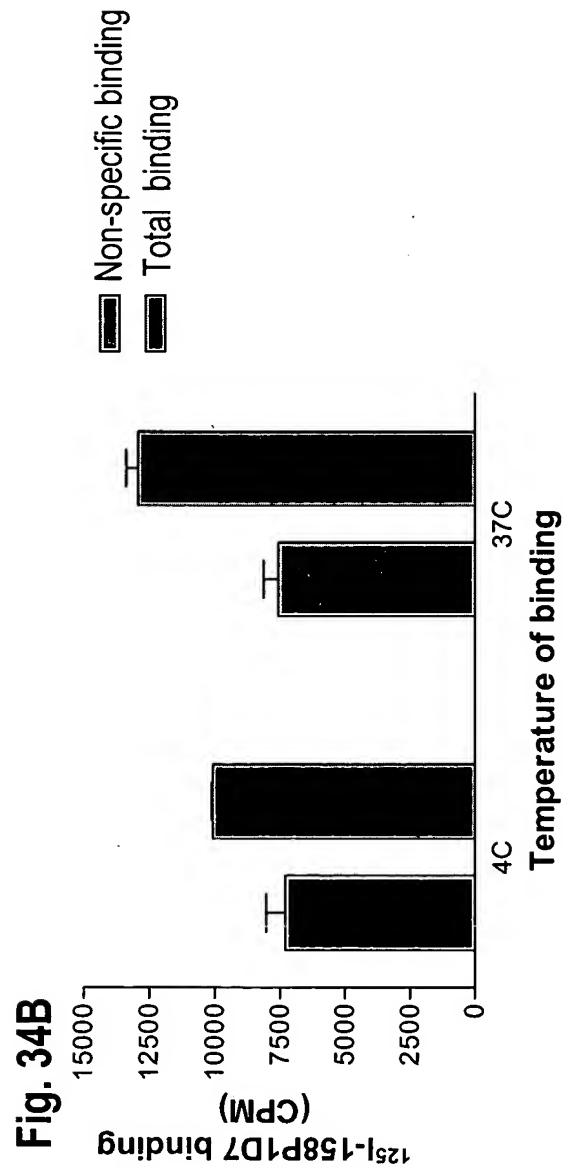


Figure 27 - 158P1D7 Enhances the Growth of Bladder Cancer UM-UC-3 Cells in Mice

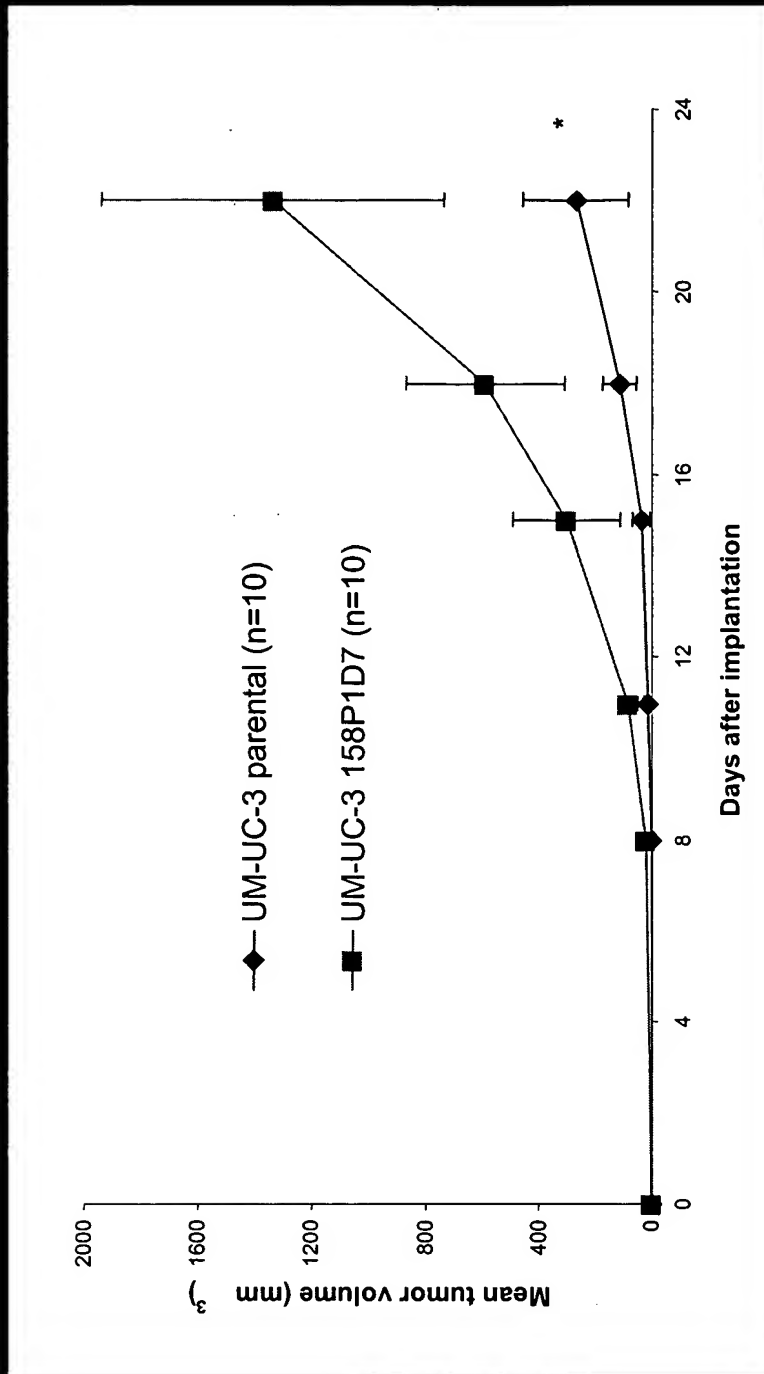


Figure 28: Internalization of MAbs M15-68(2).31.1.1 in NCI-H146 cells

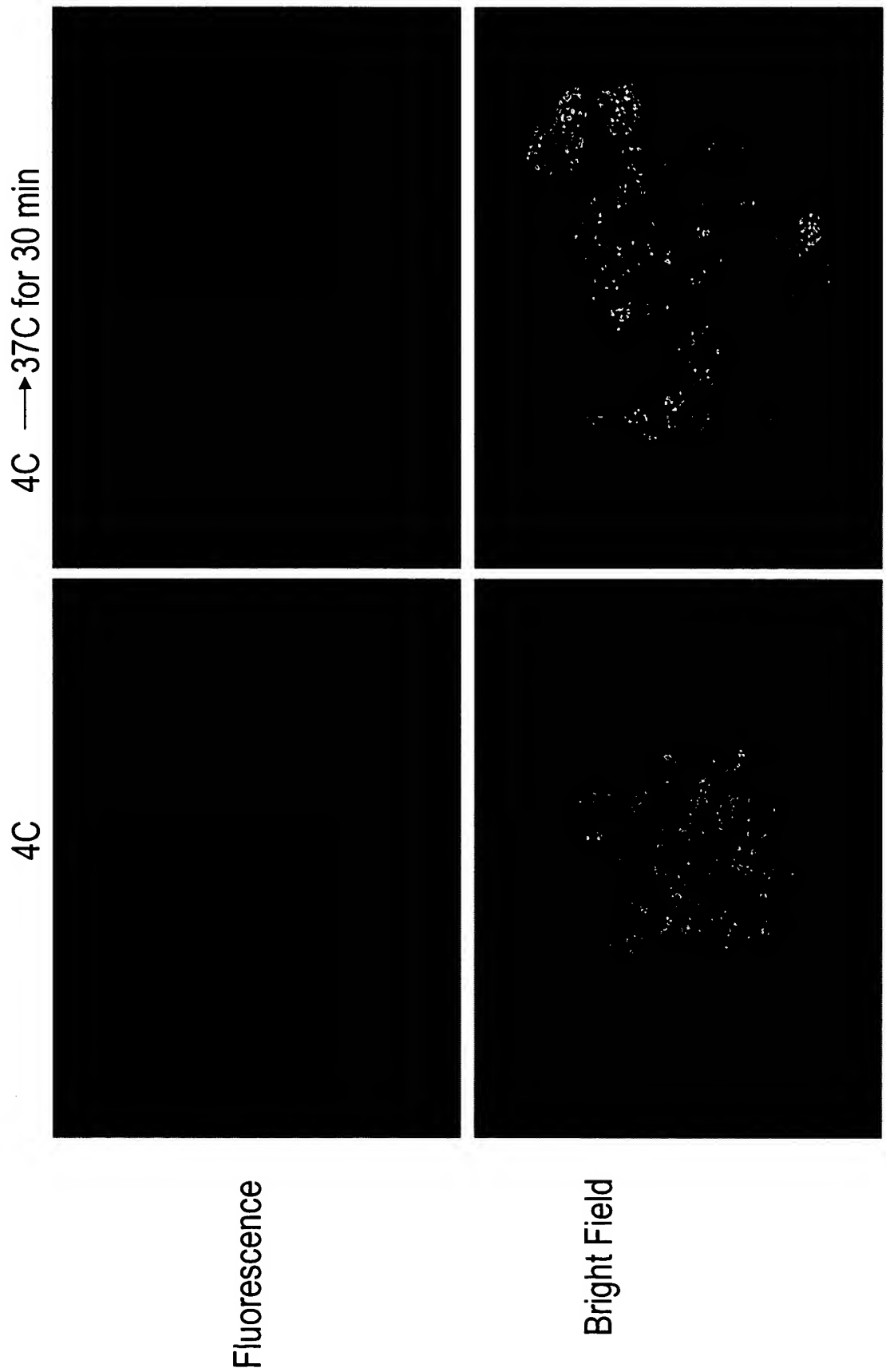


Figure 29: Effect of 158P1D7 RNAi on cell survival

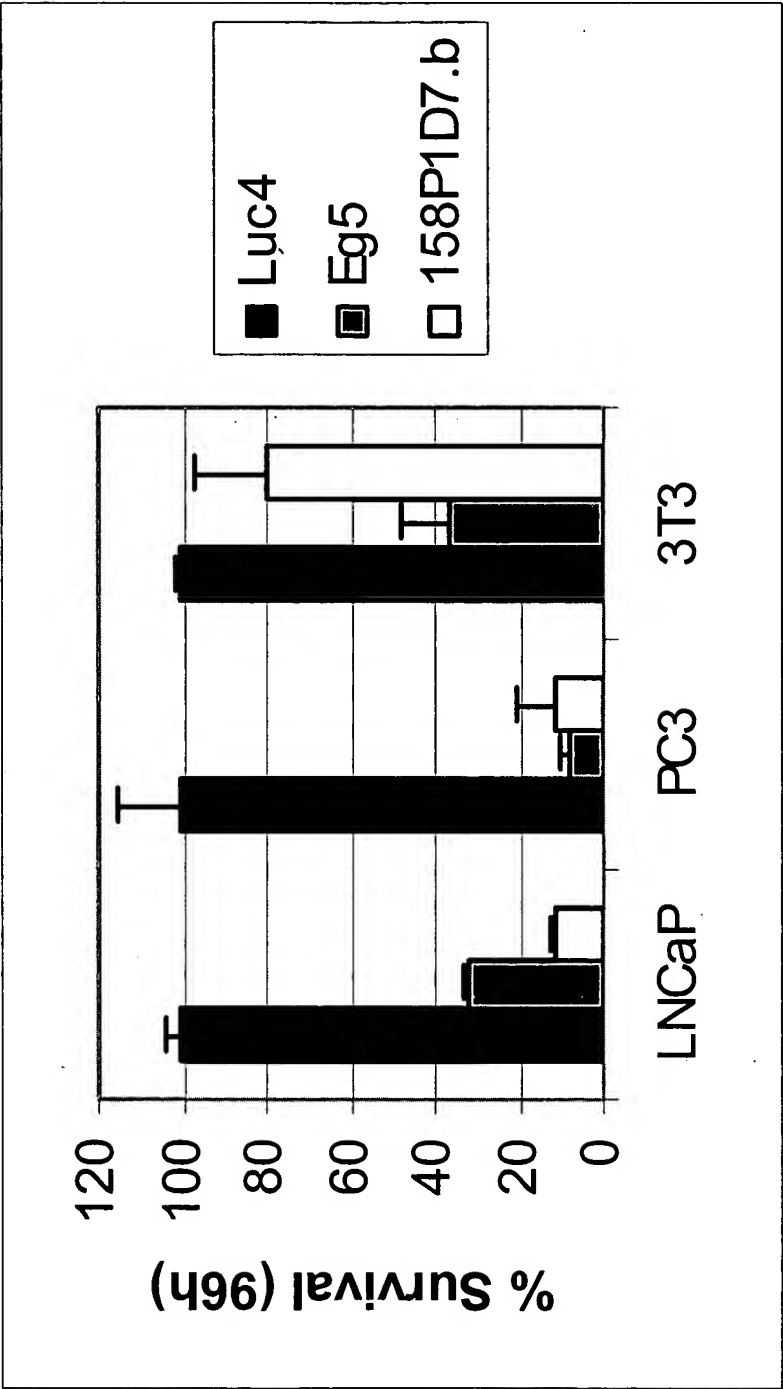


Figure 30 - 158P1D7 MAbs Retard the Growth of Human Bladder Cancer Xenografts in Mice

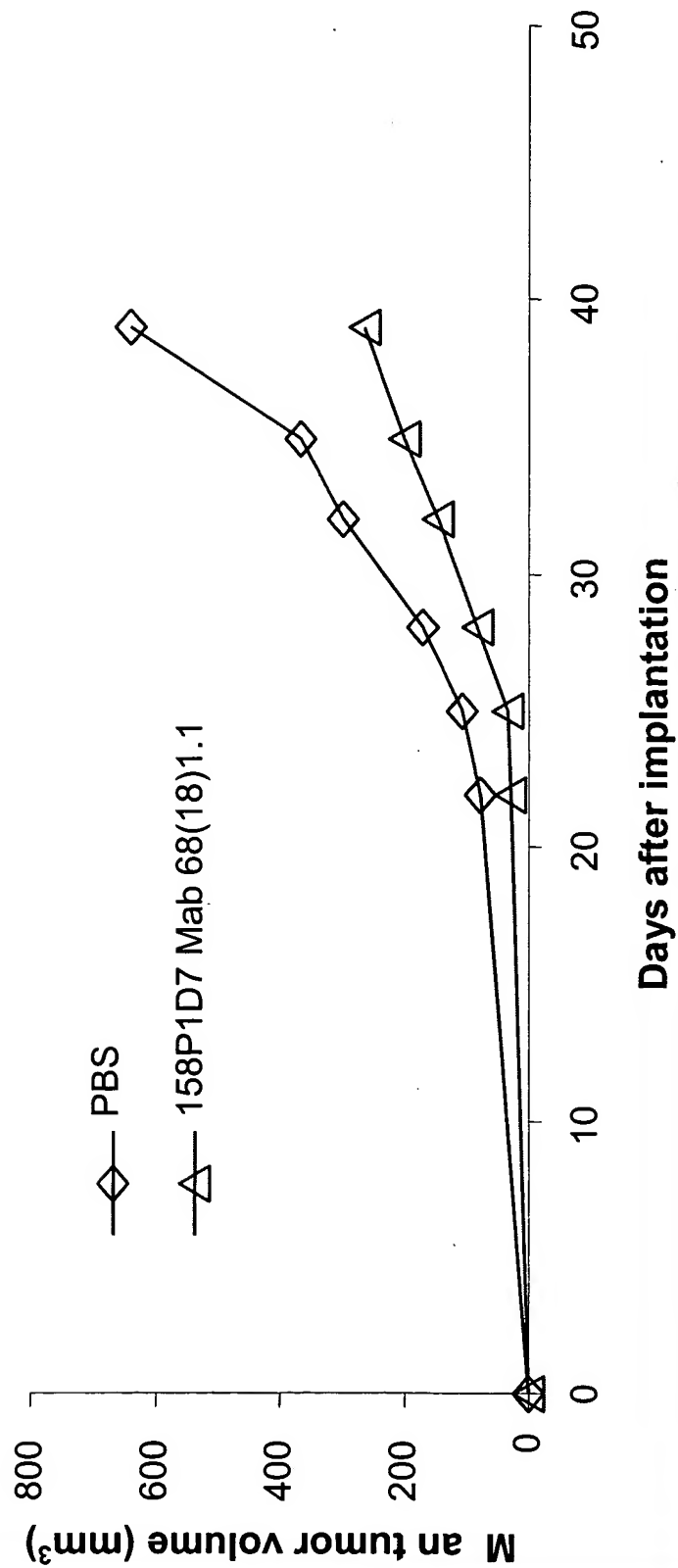


Figure 31 - 158P1D7 MAbs Retard Growth of Human Prostate Cancer Xenografts in Mice

Patient-derived LAPC9 xenograft

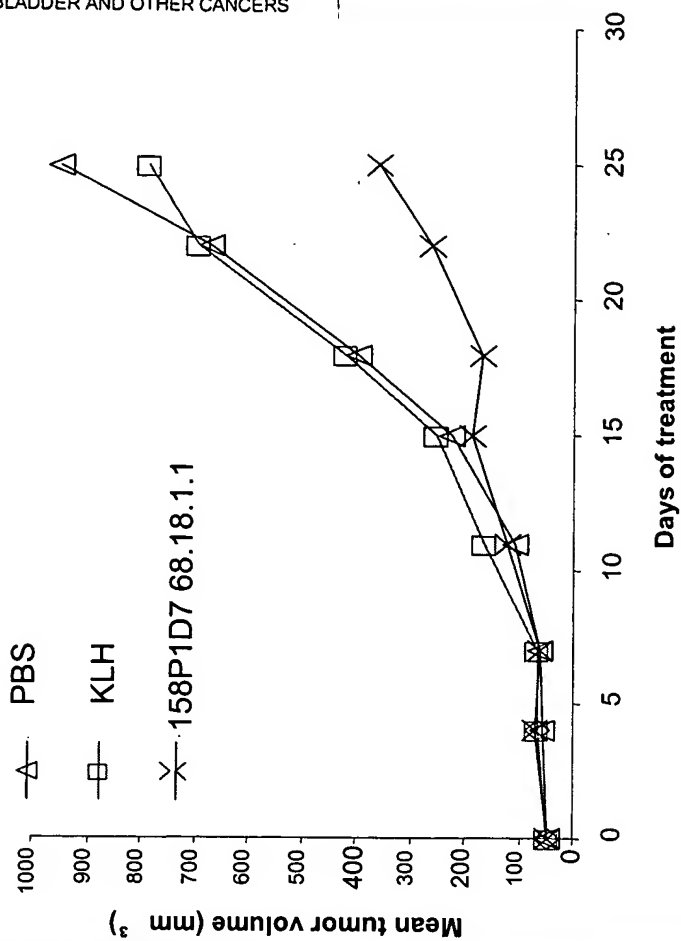
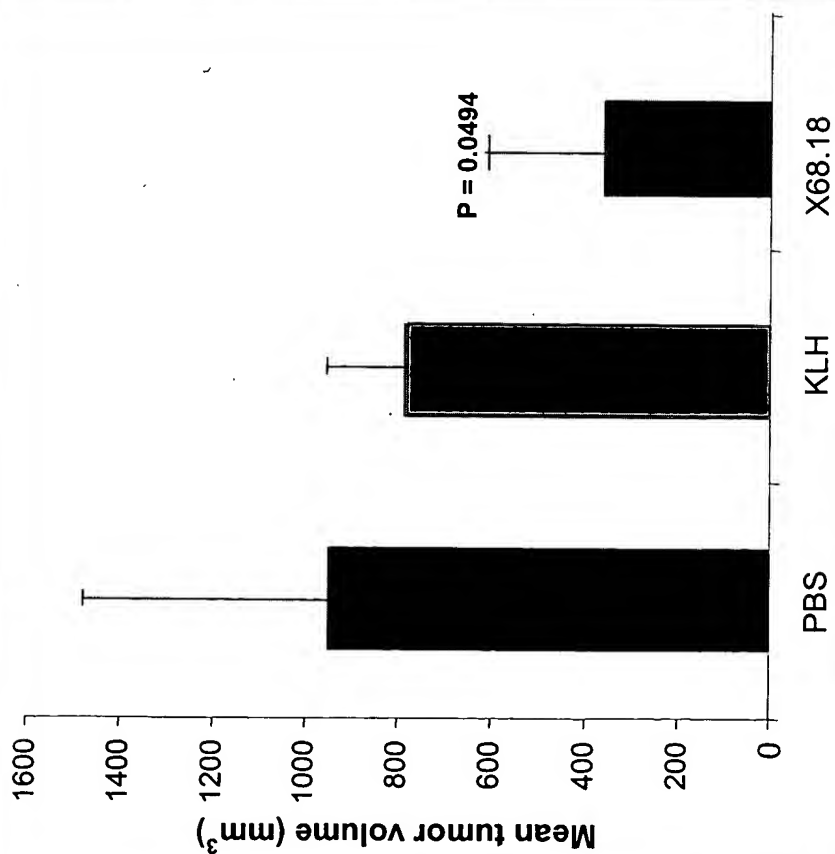


Figure 32: Effect of 158P1D7 on Proliferation of Rat1 cells

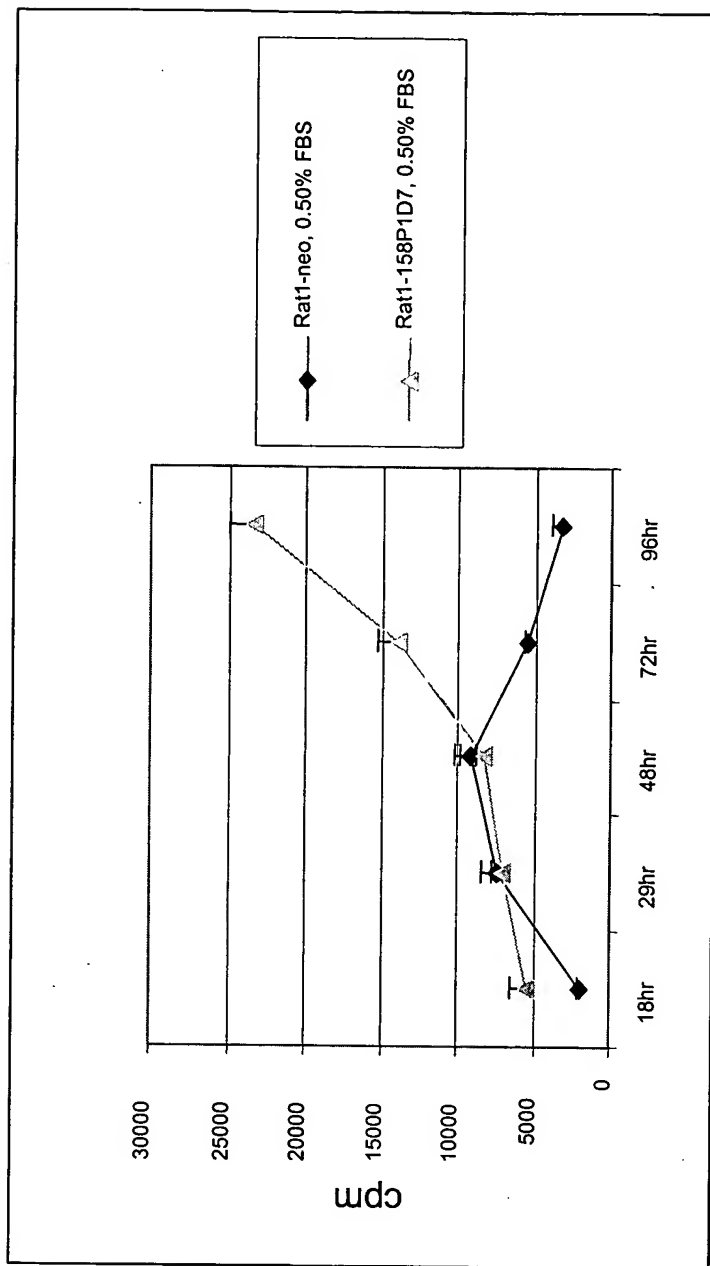


Figure 33: 158P1D7 Enhances Entry Into the S Phase

Cells	Treatment	Percent Cells		
		G1	S	G2
3T3	0.5% FBS	92.7	2.6	2.2
	10% FBS	72.8	11.4	14.7
3T3-neo	0.5% FBS	95.1	1.4	2.3
	10% FBS	59.6	14.1	18.3
3T3-158P1D7	0.5% FBS	90.1	3.3	4.4
	10% FBS	68.4	21.2	1.7

Figure 34A. The cDNA and amino acid sequence of M15/X68(2)18 VH clone #1.

```
1 Q T A G V R S W P G G A L T E P V H H M
1 caaactgcaggagtcaggagttggcctggtggcgccctcacagagcctgtccatcacatg
21 H R L R I L I D R L W C K L G S P A S R
61 caccgtctcaggattctcattgaccggctatggtgtaaactgggttcgccagcctccagg
41 K G S G V A G N D L G R W K H R L Y F S
121 aaaggtctgggggtggctgggaatgatttggggcgatggaagcacagattatacttcagc
61 S P I Q T E H Q E G Q F K S Q T F L K N
181 tctccaatccagactgagcatcaggaaggacaattcaagagccaaactttcttaaaaaat
81 N S L Q T D D T A R Y Y C A R D E G R G
241 aacagtctgcaaactgatgacacagccagggtattactgtgccagagatgaagggaggggga
101 L C L I A G A K G P R S P S P
301 ctctgtttgattgctggggccaagggaccacggtcaccgtctcctca
```

Figure 34B. The cDNA and amino acid sequence of M15/X68(2)18 VL clone #2.

```
1 D I Q L T Q S P A S L A V S L G Q R A T
1 gacattcagctgacccagtcctcctgcttccttagctgtatctctggggcagagggccacc
21 I S Y R A S K S V S T S G Y S Y M H W N
61 atctcatcacagggccagcaaaagtgtcagtacatctggctatagttatatgcactggaac
41 Q Q K P G Q P P R L L I Y L V S N L E S
121 caacagaaaccaggacagccacccagactcctcatctatcttgtatccaacctagaatct
61 G V P A R F S G S G S G T D F T L N I H
181 ggggtccctgccagggttcagtggcagtggtctgggacagacttcaccctcaacatccat
81 P V E E E D A A T Y Y C Q H I R E L T R
241 cctgtggaggaggaggatgctgcaacctattactgtcagcacattaggaggcttacacgt
101 S E G G P S W R S N
301 tcggaggggggaccaagctggagatctaac
```


Figure 35A: The amino acid sequence of M15/X68(2)18 VH clone #1.

1 QTAGVRSWPG GALTEPVHHM HRLRILIDRL WCKLGSPASR KGSGVAGNDL
51 GRWKHRLYFS SPIQTEHQEG QFKSQTFLLN NSLQTDDTAR YYCARDEGRG
101 LCLIAKAKGP RSPSP

Figure 35B: The amino acid sequence of M15/X68(2)18 VL clone #2.

1 DIQLTQSPAS LAVSLGQRAT ISYRASKSVS TSGYSYMHWN QQKPGQPPRL
51 LIYLVSNLES GVPARFSGSG SGTDFTLNIH PVVEEDAATY YCQHIRELTR
101 SEGGPSWRSN

Figure 36: Detection of 158P1D7 protein by immunohistochemistry
in various cancer patient specimens.

